


```
GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: August 26, 2005, 16:48:35 ; Search time 166 Seconds
        (without alignments)
        619.749 Million cell updates/sec

US-10-006-867-2
Title:
Perfect score: 1392
Sequence: 1 MMWFQGLSFLPSALVWITS.....YDTAPCPINNERLLSRDI 266
Scoring table: BLOSUM62

Searched:
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                Maximum Match 100%
Database :
Listing first 1500 summaries
A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
No.   Score Match Length DB ID Description
ID   AAY66636 standard; protein; 266 AA.
DE   Membrane-bound protein PRO180.
PN   W09963088-A2.
PD   09-DEC-1999.
PA   (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 1392; DB 3; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 2
ID   AAU29028 standard; protein; 266 AA.
DE   Human PRO polypeptide sequence #5.
PN   W0200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 1392; DB 4; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 3
ID   AAM39568 standard; protein; 266 AA.
DE   Human polypeptide SEQ ID NO 2713.
PN   W0200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
    Query Match 100.0%; Score 1392; DB 4; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 4
ID   AAB65159 standard; protein; 266 AA.
DE   Human PRO180 (UNQ154) protein sequence SEQ ID NO:23.
PN   W0200073454-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 1392; DB 4; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 5
ID   ABB90338 standard; protein; 266 AA.
DE   Human polypeptide SEQ ID NO 2714.
PN   W0200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
    Query Match 100.0%; Score 1392; DB 5; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 6
ID   ABG95951 standard; protein; 266 AA.
```

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DE   Human secreted/transmembrane protein PRO180.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 1392; DB 5; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 7
ID   ABUS8404 standard; protein; 266 AA.
DE   Human PRO polypeptide #5.
PN   US2003027272-A1.
PD   06-FEB-2003.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 8
ID   ABU87952 standard; protein; 266 AA.
DE   Novel human secreted and transmembrane protein PRO180.
PN   US2003032127-A1.
PD   13-FEB-2003.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 9
ID   ABU84267 standard; protein; 266 AA.
DE   Human secreted/transmembrane protein (PRO) #5.
PN   US2003032112-A1.
PD   13-FEB-2003.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 10
ID   ABR66141 standard; protein; 266 AA.
DE   Human secreted polypeptide PRO180, SEQ ID NO:10.
PN   US2003027278-A1.
PD   06-FEB-2003.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 11
ID   ABR65531 standard; protein; 266 AA.
DE   Human secreted polypeptide PRO180, SEQ ID NO:10.
PN   US2003036159-A1.
PD   20-FEB-2003.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 12
ID   ABU99471 standard; protein; 266 AA.
DE   Human secreted/transmembrane protein (PRO) #5.
PN   US2003040070-A1.
PD   27-FEB-2003.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 13
ID   ABU57974 standard; protein; 266 AA.
DE   Human PRO polypeptide #6.
PN   US2003027163-A1.
PD   06-FEB-2003.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 14
ID   ABUS9052 standard; protein; 266 AA.
DE   Novel human secreted or transmembrane protein PRO180.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 15
ID   ABU82564 standard; protein; 266 AA.
DE   Human secreted/transmembrane protein PRO180.
PN   US2003032023-A1.
PD   13-FEB-2003.
    Query Match 100.0%; Score 1392; DB 6; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 16
ID   AEU82710 standard; protein; 266 AA.
DE   Human PRO polypeptide #5.
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DE Novel human secreted and transmembrane protein PRO180.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 37
ID ABU90876 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 38
ID AB033935 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 39
ID ABR99356 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 40
ID ABR98746 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 41
ID AB016269 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 42
ID ABR92169 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 43
ID AB018810 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 44
ID ABR78231 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 45
ID ABU71952 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 46
ID ABU84967 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 47
ID ABO00106 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 48
ID ABO11438 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 49
ID ABO02083 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 50
ID ADA40898 standard; protein; 266 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 51
ID ABU88657 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 52
ID ABU83352 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 53
ID ABO06153 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 54
ID ABR59189 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 55
ID ABO09251 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 56
ID ABO19115 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 57
ID ABO11133 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 58
ID ABR66751 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 59
ID ABO15964 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 60
ID ABO13670 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 61
ID ABU71506 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180.
PN US20030113855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 62
ID ABU65573 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, SEQ ID 10.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 63
ID ABO07421 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 64
ID ABO03608 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 65
ID ABR67056 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 66
ID ABO13980 standard; protein; 266 AA.
DE Novel human secreted protein #9.
PN US2003028003-A1.
PD 06-FEB-2003.
PA (ROSE/) ROSEN C A.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJJ/) NI J.
PA (WEIY/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KYAW/) KYAW H.
PA (LAFL/) LAPLEUR D W.
PA (SHIY/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
PA (CART/) CARTER K C.
PA (BIRS/) BIRSE C E.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 67
ID ABO15659 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 68
ID ABU55940 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, PRO180.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 69
ID ABU7287 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 70
ID ABU65268 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 71
ID ABU95213 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 72
ID ABU71116 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 73
ID ABO07726 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 74
ID ABR69967 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 75
ID ABR69300 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 76
ID ABO01441 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 77
ID ABU81243 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 78
ID ABR60040 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 79
ID ABU90960 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 80
ID ABR67775 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 81
ID ABR65163 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 82
ID ABR68385 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 83
ID ABR71797 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 84

ID ABU59199 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 85
ID ABU85277 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 86
ID ABU88967 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 87
ID ABU83047 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 88
ID ABU94903 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 89
ID ABU90451 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 90
ID ABU83962 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 91
ID ABU93613 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 92
ID ABO25896 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 93
ID ABR64858 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 94
ID ABO27281 standard; protein; 266 AA.

DE Human secreted/transmembrane polypeptide PRO180.
PN US200309012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 95
ID ABR68690 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 96
ID ABO06506 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 97
ID ABR99051 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 98
ID ABU56935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 99
ID ABU58987 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 100
ID ABU82174 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 101
ID ABU87185 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 102
ID ABU83657 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 103
ID ABO08031 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 104
ID ABU92476 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003045684-A1.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 105
ID ABU81742 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 106
ID ABU65906 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 107
ID ABU81146 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 108
ID ABR59735 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 109
ID ABU93923 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 110
ID ABU99776 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 111
ID ABR66446 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 112
ID ABR90864 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 113
ID ABO53261 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 114
ID ABU58905 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.

PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 115
ID ABR64553 standard; protein; 266 AA.
DE Human secreted polypeptide #5.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 116
ID ABU79173 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 117
ID ABU86502 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 118
ID ABU86807 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 119
ID ABU94596 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 120
ID ABO04523 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 121
ID ABR70272 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 122
ID ABU92283 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 123
ID ABU98437 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 124
ID ABR65836 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036165-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 125
ID ABR64553 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 126
ID ABU59348 standard; protein; 266 AA.
DE Novel human secreted or transmembrane protein PRO180.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 127
ID ABU79478 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 128
ID ABU92869 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 129
ID ABU95828 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 130
ID ABU91048 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 131
ID ABU90141 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 132
ID ABO09556 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 133
ID ABO10828 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 134
ID ABR70882 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 135
ID ABU98263 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 136
ID ABU87490 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 137
ID ABU91358 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 138
ID ABU89268 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 139
ID ABU84572 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 140
ID ABR69662 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 141
ID ABU80039 standard; protein; 266 AA.
DE Human PRO protein #5.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 142
ID ABU92475 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 143
ID ABU92114 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 144
ID ABU93308 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 145
ID ABO09861 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 146
ID ABO08946 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 147
ID ABU96439 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 148
ID ABU10820 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 149
ID ABU10514 standard; protein; 266 AA.
DE Human secreted/transmembrane protein #5.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 150
ID ABU81572 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 151
ID ABU72109 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 152
ID ABU95523 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 153
ID ABU96732 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 154
ID ABR70577 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040076-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 155
ID ABO04928 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 156
ID ABO08336 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 157
ID ABO88511 standard; protein; 266 AA.
DE Human secreted and transmembrane polypeptide PRO180.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 158
ID ABO34025 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 159
ID ABO05543 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 160
ID ABR73932 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 161
ID ABR95524 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 162
ID ABR80821 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 163
ID ABR81126 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 164
ID ABO0822 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 165
ID ABR88424 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 166
ID ABR77245 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 167
ID ABO28729 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 168
ID ABO31474 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 169
ID ABO07891 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 170
ID ABO40371 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 171
ID ABO35796 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 172
ID ABO43935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 173
ID ADA77762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.

PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 174
ID ABR24730 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 175
ID ABO02998 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 176
ID ABR90254 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 177
ID ABR94914 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 178
ID ABR95219 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 180
ID ADB17059 standard; protein; 266 AA.
DE Human transmembrane PRO polypeptide (SeqID 2).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 181
ID ABO21457 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 182
ID ABR97721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 183
ID ABR87509 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 184
ID ABR77550 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 185
ID ABR27780 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 186
ID ABR06061 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003058704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 187
ID ABR03567 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 188
ID ABR35018 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 189
ID ABR26255 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 190
ID ABO48037 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 191
ID ABR92779 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 192
ID ABO24540 standard; protein; 266 AA.

DE Human secreted/transmembrane protein (PRO) #5.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 193
ID ADA37534 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 194
ID ABM11551 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 195
ID ABM02652 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 196
ID ABM15948 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 197
ID ABM29000 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 198
ID ABM29000 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 199
ID ABM06976 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 200
ID ABM21070 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 201
ID ABM09416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 202
ID ABO41286 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 203
ID ABO36101 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 204
ID ABO43630 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 205
ID ABM76330 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 206
ID ABM76026 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 207
ID ABM25645 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 208
ID ABM25950 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 209
ID ADA21220 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 210
ID ABO33303 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 211

ID ABO02388 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 212
ID ABO44239 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003018172-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 213
ID ABR90559 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 214
ID ABR73627 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054468-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 215
ID ABO16879 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054470-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 216
ID ABR94304 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 217
ID ABR75811 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 218
ID ABR71187 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059880-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 219
ID ABR93084 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064465-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 220
ID ABR93389 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054478-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 221
ID ADA10007 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, PRO180.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 222
ID ABR87814 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068718-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 223
ID ABO27814 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064454-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 224
ID ABO29949 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064461-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 225
ID ABO33158 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068724-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 226
ID ABO4846 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068727-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 227
ID ABO08806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068772-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 228
ID ABO36406 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068714-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 229
ID ABO35491 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068758-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 230
ID ABO39456 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 231
ID ABM10331 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 232
ID ABM11856 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 233
ID ABO52002 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 234
ID ABO52307 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 235
ID ADA19864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 236
ID ABO23625 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 237
ID ADB17247 standard; protein; 266 AA.
DE Human transmembrane PRO polypeptide (SeqID 2).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 238
ID ADA17551 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 239
ID ABR97111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 240
ID ABR86899 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 241
ID ABM10941 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 242
ID ABM28085 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 243
ID ABO32084 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 244
ID ABM15211 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003088692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 245
ID ABM08366 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 246
ID ABM04177 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 247
ID ABM22290 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 248
ID ABM07586 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068751-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 249
ID ABO40676 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 250
ID ABR35223 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 251
ID ABR3086 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 252
ID ABO52612 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 253
ID ABO50172 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 254
ID ABU99166 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 255
ID ABO04218 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 256
ID ABO05848 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 257
ID ABR18388 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 258
ID ADA27659 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 259
ID ABR97416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 260
ID ABR80516 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 261
ID ABR01127 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 262
ID ABR88729 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 263
ID ABR13381 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 264
ID ABR20765 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 265
ID ABO41896 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 266
ID ABO42506 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 267
ID ABR10026 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003067478-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 268
ID ABO38541 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 269
ID ABM32781 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 270
ID ABM22595 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 271
ID ABM74806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 272
ID ADA79554 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 273
ID ABR96196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 274
ID ABM02347 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 275
ID ABR86289 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 276
ID ABR86594 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 277

ID ABM16558 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 278
ID ABM29610 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 279
ID ABO29034 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 280
ID ABM23815 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 281
ID ABM23205 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 282
ID ABM21985 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 283
ID ABO37626 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 284
ID ABM28390 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 285
ID ABM28695 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 286
ID ABM66339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068737-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 287
ID ABM75721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 288
ID ABM34001 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 289
ID ABM34306 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 290
ID ABO20237 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 291
ID ABO21152 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 292
ID ABO22067 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 293
ID ADA20036 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 294
ID ABO34167 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 295
ID ABR96501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 296
ID ADA94239 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 297
ID ABR85679 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 298
ID ABR99661 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 299
ID ABM00212 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 300
ID ABM00517 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 301
ID ABO29644 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 302
ID ABM23510 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 303
ID ABM29305 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 304
ID ABO38236 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 305
ID ABO45536 standard; protein; 266 AA.
DE Human PRO polypeptide #5.

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PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 306
ID ABM20460 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 307
ID ADA81281 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 308
ID ABO16574 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 309
ID ABO18200 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 310
ID ABO22627 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 311
ID ABO22932 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 312
ID ABR92474 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 313
ID ABR81431 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 314
ID ABM77855 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 315
ID ABR89644 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 316
ID ABM26560 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 317
ID ABM13686 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 318
ID ABO28424 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 319
ID ABO30254 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 320
ID ABM07281 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 321
ID ABM03872 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 322
ID ABO37016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 323
ID ABO41591 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 324
ID ABO35186 standard; protein; 266 AA.
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DE Human PRO polypeptide #5.
PN US2003068738-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 325
ID ABO17895 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 335
ID ABO20847 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 336
ID ABR96806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 337
ID ADA38464 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 338
ID ABM12161 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 339
ID ABM16253 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 340
ID ABM24120 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 341
ID ABM14601 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003086696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 342
ID ABM04482 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 343
ID ABM06671 standard; protein; 266 AA.

DE Human PRO polypeptide #5.
PN US2003068738-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 325
ID ABR25035 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 326
ID ABO47427 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 327
ID ABO47732 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 328
ID ABO48342 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 329
ID ABO51392 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 330
ID ABO51697 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 331
ID ABO50477 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 332
ID ABR79601 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 333
ID ABM16863 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040078-A1.
PD 27-FEB-2003.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
ID ABR72102 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 354
ID ABR98441 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 355
ID ABO06811 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PD US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 356
ID ABR84764 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 357
ID ABR73322 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 358
ID ABR76416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 359
ID ABR73017 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 360
ID ABM18083 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 361
ID ABO20542 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PD US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 362
ID ABO25285 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PD US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
ID ABR72102 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 344
ID ABM09111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 345
ID ABO39151 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PD US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 346
ID ABM75416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 347
ID ABM25340 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 348
ID ABM19850 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 349
ID ABO46756 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PD US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 350
ID ABO47061 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PD US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 351
ID ADA83079 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PD US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 352
ID ABR71492 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003032133-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 363
ID ABO25590 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 364
ID ABR93999 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 365
ID ADA92585 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 366
ID ABR79906 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 367
ID ABM11246 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 368
ID ABO32853 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 369
ID ABO30559 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 370
ID ABO30864 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 371
ID ABM27170 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 372
ID ABM19545 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

ID ABM29915 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 373
ID ABM05451 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 374
ID ABM15516 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 375
ID ABM08501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 376
ID ABO42201 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 377
ID ABO37931 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 378
ID ABO45841 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 379
ID ABM66644 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 380
ID ADB20122 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 381
ID ABM19545 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003104552-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 382
ID ABO49257 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 383
ID ABO49562 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 384
ID ADA78374 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 385
ID ABR88119 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 386
ID ADA00333 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 387
ID ABM26865 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 388
ID ABM03262 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 389
ID ABO39761 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 390
ID ABO49867 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049776-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 391
ID ABO50782 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 392
ID ABO5238 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 393
ID ABR74542 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 394
ID ABR77021 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 395
ID ABM17778 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 396
ID ABR95829 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 397
ID ABO21762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 398
ID ABO19932 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 399
ID ABO24235 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 400
ID ABR85984 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003049759-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 401
ID ABRM10636 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 402
ID ABRM76635 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 403
ID ABR89339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 404
ID ABRM12466 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 405
ID ABRM05756 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 406
ID ABR034881 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 407
ID ABRM02957 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 408
ID ABRM18935 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 409
ID ABRM19240 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104551-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 410
ID ABR046451 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 411
ID ABR048952 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 412
ID ABR68995 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 413
ID ABR89034 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 414
ID ABR72407 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 415
ID ABR74237 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 416
ID ABR018505 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 417
ID ABR80211 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 418
ID ABRM01432 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059862-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 419
ID ABRM02042 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 420
ID ABR87204 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 421
ID ABM12771 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 422
ID ABM30525 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 423
ID ABM24425 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 424
ID ABO29339 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 425
ID ABO31169 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 426
ID ABM14296 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 427
ID ABM09721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 428
ID ABO38846 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 429
ID ABR34611 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 430
ID ABO51087 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 431
ID ABO03913 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 432
ID ABO10383 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 433
ID ABO53111 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 434
ID ABR77626 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 435
ID ABR78836 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 436
ID ABO23930 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 437
ID ABR93694 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 438
ID ABM01737 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 439
ID ASW78160 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 440
ID ABR89949 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 441
ID ADA22146 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 442
ID ABM27475 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 443
ID ABM13076 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 444
ID ABO31779 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 445
ID ABM13991 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 446
ID ASW08196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 447
ID ABO40066 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 448
ID ABM74501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 449
ID ABM33696 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 450
ID ABM20155 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 451
ID ABO48647 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 452
ID ABO22481 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 453
ID ABR72712 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 454
ID ABO15354 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 455
ID ABR85069 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 456
ID ABO15049 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 457
ID ABO17184 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.

PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 458
ID ABM17473 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 459
ID ADA06312 standard; protein; 266 AA.
DE Human secreted/transmembrane PRO polypeptide #6.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 460
ID ADA39005 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 461
ID ABR85374 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 462
ID ABR76940 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 463
ID ABO28119 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 464
ID ABM22900 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 465
ID ABM30220 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 466
ID ABM21680 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 467
ID ABM21375 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 468
ID ABM14906 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 469
ID ABO40981 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 470
ID ABO36711 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 471
ID ABO37321 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 472
ID ABO75111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 473
ID ABM33391 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 474
ID ABO46146 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 475
ID ADA82445 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 476
ID ABO37321 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

ID ADB85575 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 477
ID ADB96031 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 478
ID ADB31745 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 479
ID ADB31135 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 480
ID ADB85753 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 481
ID ADB32050 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 482
ID ADB32355 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 483
ID ADB68254 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 484
ID ADB68061 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 485
ID ADB31440 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068761-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 486
ID ADB30830 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 487
ID ADB90878 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 488
ID ADC57503 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 489
ID ADC54867 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 490
ID ADC11734 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 491
ID ADC06958 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003050602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 492
ID ADC56156 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 493
ID ADC17137 standard; protein; 266 AA.
DE Mammalian PRO polypeptide (SeqID 2).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 494
ID ADC07211 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 495
ID ADC11201 standard; protein; 266 AA.

DE Human secreted/transmembrane protein PRO180.
PN US2003069403-A1.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 496
ID ADC14835 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 497
ID ADC52330 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 498
ID ADC14323 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 499
ID ADD07855 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 500
ID ADC81680 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 501
ID ADD07322 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 502
ID ADC82213 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 503
ID ADD05483 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 504
ID ADC78249 standard; protein; 266 AA.
DE Human secreted protein SEQ ID NO:56.
PN WO2003072761-A1.
PD 04-SEP-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 505
ID ADD08393 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 506
ID ADD06642 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 507
ID ADC82889 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 508
ID ADD54996 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 509
ID ADD36006 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 510
ID ADD55954 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 511
ID ADD54392 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 512
ID ADE26546 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 513
ID ADE26013 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 514
ID ADF66950 standard; protein; 266 AA.
DE Human PRO180 amino acid sequence SEQ ID NO:23.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;

DE Novel human secreted and transmembrane protein PRO180.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 534
ID ADH38498 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 535
ID ADG83619 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 536
ID ADH29427 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 537
ID ADH27543 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 538
ID ADH37740 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 539
ID ADH37917 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 540
ID ADH57337 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 541
ID ADH53479 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 542
ID ADH53649 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 543
ID ADH51985 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 544
ID ADH49840 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 545
ID ADI25350 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 546
ID ADH90143 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 547
ID ADI25520 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 548
ID ADH97694 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 549
ID ADI35204 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 550
ID ADI03542 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 551
ID ADI11899 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181686-A1.
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 552
ID ADH98973 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 553
ID ADH99696 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 554
ID ADH98374 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 555
ID ADI11049 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 556
ID ADI11559 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 557
ID ADH98204 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 558
ID ADH98544 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 559
ID ADH98034 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 560
ID ADI05022 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 561
ID ADI03372 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 562
ID ADI04767 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 563
ID ADH78221 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 564
ID ADI19565 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 565
ID ADH90313 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 566
ID ADI03032 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 567
ID ADH77881 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 568
ID ADH97864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 569
ID ADI01249 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
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ID ADH79608 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
FN US2003191288-A1.
PA 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 580
ID ADI01434 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
FN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 581
ID ADI01604 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
FN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 582
ID ADI01774 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
FN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 583
ID ADH79778 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
FN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 584
ID ADI04596 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
FN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 585
ID ADI02732 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
FN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 586
ID ADH78051 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
FN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 587
ID ADI25690 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
FN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match Similarity 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 588
ID ADI25860 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 589
ID ADK65372 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 590
ID ADH98714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 591
ID ADH79955 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 592
ID ADL32616 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 593
ID ADM30150 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 594
ID ADL93686 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 595
ID ADC52140 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 596
ID ADE74147 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 597
ID ADE74759 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003211574-A1.

PD 13-NOV-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 598
ID ADF35149 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 599
ID ADG11399 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 600
ID ADF95972 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 601
ID ADG04243 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 602
ID ADG00403 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 603
ID ADH06572 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 604
ID ADH06402 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 605
ID ADG68823 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 606
ID ADH27713 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

DE Novel human secreted and transmembrane protein PRO180.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 626
ID ADH33516 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 627
ID ADH33856 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 628
ID ADH01066 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 629
ID ADG69673 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 630
ID ADH20762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 631
ID ADH02159 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 632
ID ADG69163 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 633
ID ADG85948 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 634
ID ADH24884 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180909-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 635
ID ADH39501 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 636
ID ADH19802 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 637
ID ADH02499 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 638
ID ADG68993 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 639
ID ADH07596 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 640
ID ADG86118 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 641
ID ADH24714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 642
ID ADH25762 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 643
ID ADH33328 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180922-A1.
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 644
ID ADH57167 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 645
ID ADH52155 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 646
ID ADH49521 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 647
ID ADH90483 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 648
ID ADI11219 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 649
ID ADH98884 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 650
ID ADI02114 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 651
ID ADH90653 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 652
ID ADU54648 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 653
ID ADJ98528 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 654
ID ADJ98698 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 655
ID ADH78857 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 656
ID ADJ99091 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 657
ID ADJ99261 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 658
ID ADJ98879 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 659
ID ADH79027 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 660
ID ADK00887 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 661
ID ADK14408 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 662
ID ADJ64419 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 663
ID ADM31315 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 664
ID ADM36362 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 665
ID ADM40167 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 666
ID ADM80857 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 667
ID ADM60677 standard; protein; 266 AA.
DE Human secreted polypeptide #9.
PN US2004038277-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 668
ID ADM37775 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 669
ID AAY27575 standard; protein; 267 AA.
DE Human secreted protein encoded by gene No. 9.
PN WO9924836-A1.
PD 20-MAY-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 670
ID ADG78386 standard; protein; 267 AA.
DE Human secreted protein #9.
PN US2003211472-A1.
PD 13-NOV-2003.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
Query Match 77.4%; Score 1078; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
RESULT 671
ID ABB12041 standard; peptide; 275 AA.
DE Human secreted protein homologue, SEQ ID NO:2411.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSB-) HYSEQ INC.
Query Match 100.0%; Score 1392; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
RESULT 672
ID AAM41354 standard; protein; 275 AA.
DE Human polypeptide SEQ ID NO 6285.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSB-) HYSEQ INC.
Query Match 100.0%; Score 1392; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
RESULT 673
ID AAB87526 standard; protein; 266 AA.
DE Human PRO180.
PN WO200118318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1390; DB 4; Length 266;
Best Local Similarity 99.6%; Pred. No. 6.9e-149;
RESULT 674
ID AAY36185 standard; protein; 267 AA.
DE Human secreted protein #57.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 99.7%; Score 1388; DB 2; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.2e-148;
RESULT 675
ID ADJ46037 standard; protein; 267 AA.
DE Novel human secreted protein-related protein sequence SeqID190.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCU/) DUCLETT A.
PA (BOUG/) BOUGUELERET L.
Query Match 99.7%; Score 1388; DB 7; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.2e-148;
RESULT 676
ID ADP19446 standard; protein; 267 AA.
DE Human secreted polypeptide #297.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 99.7%; Score 1388; DB 8; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.2e-148;
RESULT 677
ID AAY29866 standard; protein; 208 AA.
DE Human secreted protein clone pe318_4.
PN WO9946287-A1.
PD 16-SEP-1999.
PA (GEMY) GENETICS INST INC.
Query Match 77.4%; Score 1078; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
RESULT 678

ID ABP75476 standard; protein; 166 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 660.
PN WO200238376-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 58.6%; Score 816; DB 6; Length 166;
Best Local Similarity 93.4%; Pred. No. 5.7e-84;
RESULT 679
ID AAB88330 standard; protein; 136 AA.
DE Human membrane or secretory protein clone PSEC0031.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 52.1%; Score 725; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 9.3e-74;
RESULT 680
ID AAY36138 standard; protein; 172 AA.
DE Human secreted protein #10.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 42.8%; Score 595.5; DB 2; Length 172;
Best Local Similarity 79.4%; Pred. No. 6.6e-59;
RESULT 681
ID ADJ45943 standard; protein; 172 AA.
DE Novel human secreted protein-related protein sequence SeqID96.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 42.8%; Score 595.5; DB 7; Length 172;
Best Local Similarity 79.4%; Pred. No. 6.6e-59;
RESULT 682
ID ADM04182 standard; protein; 238 AA.
DE Human protein of the invention SEQ ID NO:2867.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 34.9%; Score 486.5; DB 7; Length 238;
Best Local Similarity 38.6%; Pred. No. 2.5e-46;
RESULT 683
ID AAE26425 standard; protein; 231 AA.
DE Human transmembrane protein (TMP)-11 protein.
PN WO200234783-A2.
PD 02-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 34.5%; Score 480.5; DB 5; Length 231;
Best Local Similarity 38.7%; Pred. No. 1.1e-45;
RESULT 684
ID ADK70499 standard; protein; 231 AA.
DE Respiratory disease differentially expressed protein #65.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 34.5%; Score 480.5; DB 8; Length 231;
Best Local Similarity 38.7%; Pred. No. 1.1e-45;
RESULT 685
ID AAE05342 standard; protein; 238 AA.
DE Mouse secreted protein #1.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 34.4%; Score 479.5; DB 4; Length 238;
Best Local Similarity 37.3%; Pred. No. 1.5e-45;
RESULT 686
ID ABQ00865 standard; protein; 246 AA.
DE Polypeptide encoded by novel human contig #116.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 33.2%; Score 461.5; DB 6; Length 246;
Best Local Similarity 39.3%; Pred. No. 1.8e-43;
RESULT 687
ID ABB60356 standard; protein; 246 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7860.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 26.0%; Score 361.5; DB 4; Length 246;
Best Local Similarity 33.6%; Pred. No. 4.1e-32;
RESULT 688
ID AAY36219 standard; protein; 69 AA.
DE Human secreted protein #91.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 689
ID AAY36172 standard; protein; 69 AA.
DE Human secreted protein #44.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 690
ID ADJ46071 standard; protein; 69 AA.
DE Novel human secreted protein-related protein sequence SeqID224.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 691
ID ADJ45977 standard; protein; 69 AA.
DE Novel human secreted protein-related protein sequence SeqID130.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 692
ID ADP19480 standard; protein; 69 AA.
DE Human secreted polypeptide #331.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 25.7%; Score 358; DB 8; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 693
ID ABE28122 standard; protein; 200 AA.
DE Novel human diagnostic protein #28113.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.6%; Score 356.5; DB 4; Length 200;
Best Local Similarity 74.0%; Pred. No. 1.1e-31;
RESULT 694
ID ABB97776 standard; protein; 85 AA.
DE Human secretory polypeptide (SPTM) 28.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 25.6%; Score 356; DB 5; Length 85;
Best Local Similarity 86.1%; Pred. No. 4e-32;
RESULT 695
ID AAY04148 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO:19.
PN WO9906439-A2.
PD 11-FEB-1999.

PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 696
 ID AAW93616 standard; protein; 69 AA.
 DE Human 5' EST secreted protein clone 58-34-2-E7-FL2.
 PN W09906551-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 697
 ID AAY04166 standard; protein; 69 AA.
 DE Human 5' EST secreted protein SEQ ID NO:19.
 PN W09906548-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 698
 ID AAY35882 standard; protein; 69 AA.
 DE Extended human secreted protein sequence, SEQ ID NO. 19.
 PN W09931236-A2.
 PD 24-JUN-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 699
 ID AAY59645 standard; protein; 69 AA.
 DE Secreted protein extended EST protein sequence #2.
 PN W09940189-A2.
 PD 12-AUG-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 700
 ID AAY01590 standard; protein; 69 AA.
 DE Secreted protein encoded by an extended 5' EST cDNA sequence.
 PN W09906554-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 701
 ID AAY12982 standard; protein; 69 AA.
 DE Human secreted protein encoded by 5' EST clone 58-34-2-E7-FL2.
 PN W09906552-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 702
 ID AAY25451 standard; protein; 69 AA.
 DE Human secreted protein 2 derived from extended cDNA.
 PN W09925825-A2.
 PD 27-MAY-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 703
 ID AAY12672 standard; peptide; 69 AA.
 DE Human 5' EST secreted protein.
 PN W09906549-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 25.3%; Score 352; DB 2; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 704
 ID AAG00010 standard; protein; 69 AA.
 DE Human secreted protein #1.
 PN EP1033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.

Query Match 25.3%; Score 352; DB 3; Length 69;
 Best Local Similarity 98.5%; Pred. No. 8.5e-32;
 RESULT 705
 ID ABB89768 standard; protein; 180 AA.
 DE Human polypeptide SEQ ID NO 2144.
 PN W0200190304-A2.
 PD 29-NOV-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.8%; Score 317.5; DB 5; Length 180;
 Best Local Similarity 33.3%; Pred. No. 2.6e-27;
 RESULT 706
 ID AAG81279 standard; protein; 114 AA.
 DE Human AFP protein sequence SEQ ID NO:76.
 PN W0200129221-A2.
 PD 26-APR-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 19.6%; Score 272.5; DB 4; Length 114;
 Best Local Similarity 47.5%; Pred. No. 1.8e-22;
 RESULT 707
 ID AAB93632 standard; protein; 132 AA.
 DE Human protein sequence SEQ ID NO:13115.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 18.0%; Score 251; DB 4; Length 132;
 Best Local Similarity 33.3%; Pred. No. 6.1e-20;
 RESULT 708
 ID ADL06520 standard; protein; 132 AA.
 DE Human tumour-associated antigenic target (TAT) polypeptide #19.
 PN W02004016225-A2.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 18.0%; Score 251; DB 8; Length 132;
 Best Local Similarity 33.3%; Pred. No. 6.1e-20;
 RESULT 709
 ID ADJ75472 standard; protein; 132 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:724.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match 18.0%; Score 251; DB 8; Length 132;
 Best Local Similarity 33.3%; Pred. No. 6.1e-20;
 RESULT 710
 ID ADR14452 standard; protein; 132 AA.
 DE Human NF-kappaB pathway-associated protein SeqID453.
 PN W02004065577-A2.
 PD 05-AUG-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 18.0%; Score 251; DB 8; Length 132;
 Best Local Similarity 33.3%; Pred. No. 6.1e-20;
 RESULT 711
 ID ADP24981 standard; protein; 132 AA.
 DE PRO polypeptide SEQ ID NO:2159.
 PN W02004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 18.0%; Score 251; DB 8; Length 132;
 Best Local Similarity 33.3%; Pred. No. 6.1e-20;
 RESULT 712
 ID ADS11008 standard; protein; 233 AA.
 DE Human therapeutic protein - SEQ ID 1245.
 PN W02004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 15.8%; Score 220.5; DB 8; Length 233;
 Best Local Similarity 27.2%; Pred. No. 3.9e-16;
 RESULT 713
 ID ABO00507 standard; protein; 283 AA.
 DE Novel human polypeptide #94.
 PN W02003023013-A2.
 PD 20-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 15.4%; Score 214.5; DB 6; Length 283;

ID ABO00615 standard; protein; 63 AA.
DE Novel human polypeptide #20.
PD WO2003023013-A2.
PN 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 9.1%; Score 126; DB 6; Length 63;
Best Local Similarity 47.2%; Pred. No. 3.5e-06;
RESULT 733
ID A0S11007 standard; protein; 127 AA.
DE Human therapeutic protein - SEQ ID 1244.
PD WO2004080148-A2.
PN 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 8.8%; Score 122.5; DB 8; Length 127;
Best Local Similarity 32.1%; Pred. No. 2.3e-05;
RESULT 734
ID AAY04149 standard; peptide; 21 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
PD WO9906439-A2.
PN 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 735
ID AAY11369 standard; protein; 21 AA.
DE Human 5' EST secreted protein SEQ ID NO:20.
PD WO9908551-A2.
PN 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 736
ID AAY12516 standard; peptide; 21 AA.
DE Human 5' EST signal peptide SEQ ID NO: 20 from WO 9906553.
PD WO9906553-A2.
PN 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 737
ID AAY35883 standard; peptide; 21 AA.
DE Signal peptide of extended secreted protein, SEQ ID NO. 20.
PD WO9931236-A2.
PN 24-JUN-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 738
ID AAY59644 standard; peptide; 21 AA.
DE Secreted protein extended EST signal peptide #2.
PD WO9940189-A2.
PN 12-AUG-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 739
ID AAY25452 standard; peptide; 21 AA.
DE Human secreted protein 2 signal peptide derived from extended cDNA.
PD WO9925825-A2.
PN 27-MAY-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 740
ID AAY12671 standard; peptide; 21 AA.
DE Human 5' EST secreted protein signal peptide.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 741
ID AAY11711 standard; protein; 21 AA.
DE Peptide encoded by extended cDNA derived from 5' EST.
PD WO9906550-A2.
PN 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 742
ID AAY64644 standard; peptide; 21 AA.
DE Human 58-34-2-E7-FL2 signal peptide.
PD WO9953051-A2.
PN 21-OCT-1999.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 743
ID AAG00011 standard; peptide; 21 AA.
DE Human secreted protein #1 signal peptide.
PD EP1033401-A2.
PN 06-SEP-2000.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 744
ID AAO20328 standard; peptide; 21 AA.
DE Signal peptide encoded by the cDNA 58-34-2-E7-FL2.
PN CA2343602-A1.
PD 18-OCT-2001.
PA (GEST-) GENSET.
Query Match 8.5%; Score 118; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 745
ID ADJ45867 standard; peptide; 21 AA.
DE Novel human secreted protein-related peptide sequence SeqID20.
PD US200314490-A1.
PN 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 8.5%; Score 118; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 746
ID ADM77739 standard; peptide; 21 AA.
DE Signal sequence #2.
PD US2003162176-A1.
PN 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 8.5%; Score 118; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 747
ID AAY04167 standard; peptide; 21 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
PD WO9906548-A2.
PN 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 8.1%; Score 113; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.3e-05;
RESULT 748
ID AAU04087 standard; peptide; 21 AA.
DE Signal peptide encoded by Human cDNA 58-34-2-E7-FL2.
PD EP1104808-A1.
PN 06-JUN-2001.
PA (GEST-) GENSET.
Query Match 8.1%; Score 113; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 749
ID ABB60233 standard; protein; 275 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7491.
PD WO200171042-A2.
PN 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.7%; Score 106.5; DB 4; Length 275;

Best Local Similarity 21.3%; Pred. No. 0.0044;
RESULT 750
ID AAB38499 standard; peptide; 220 AA.
DE Fragment of human secreted protein encoded by gene 53 clone HFABG18.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.5%; Score 105; DB 3; Length 220;
Best Local Similarity 22.8%; Pred. No. 0.0048;
RESULT 751
ID AAM93195 standard; protein; 218 AA.
DE Human polypeptide, SEQ ID NO: 2575.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.3%; Score 101; DB 4; Length 218;
Best Local Similarity 22.8%; Pred. No. 0.013;
RESULT 752
ID ADL30542 standard; protein; 218 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2575.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 101; DB 8; Length 218;
Best Local Similarity 22.8%; Pred. No. 0.013;
RESULT 753
ID ADM06102 standard; protein; 187 AA.
DE Human protein of the invention SEQ ID NO:4787.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.1%; Score 99; DB 7; Length 187;
Best Local Similarity 23.4%; Pred. No. 0.018;
RESULT 754
ID ABU45347 standard; protein; 1066 AA.
DE Protein encoded by Prokaryotic essential gene #30874.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1066;
Best Local Similarity 19.5%; Pred. No. 0.23;
RESULT 755
ID ABU47563 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #33090.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1120;
Best Local Similarity 19.5%; Pred. No. 0.24;
RESULT 756
ID ABU46980 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #32507.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1120;
Best Local Similarity 19.5%; Pred. No. 0.24;
RESULT 757
ID ABU34113 standard; protein; 548 AA.
DE Protein encoded by Prokaryotic essential gene #19640.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.8%; Score 94.5; DB 6; Length 548;
Best Local Similarity 18.2%; Pred. No. 0.26;
RESULT 758
ID ABU39811 standard; protein; 269 AA.
DE Protein encoded by Prokaryotic essential gene #25338.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.8%; Score 94; DB 6; Length 269;
Best Local Similarity 21.7%; Pred. No. 0.11;

RESULT 759
ID AAG44537 standard; protein; 303 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55801.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 93.5; DB 3; Length 303;
Best Local Similarity 21.8%; Pred. No. 0.15;
RESULT 760
ID AAG44536 standard; protein; 367 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55800.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 93.5; DB 3; Length 367;
Best Local Similarity 21.8%; Pred. No. 0.19;
RESULT 761
ID ABU15091 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #618.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 93; DB 6; Length 1120;
Best Local Similarity 19.6%; Pred. No. 1;
RESULT 762
ID ABU47616 standard; protein; 473 AA.
DE Protein encoded by Prokaryotic essential gene #33143.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.8%; Score 92.5; DB 6; Length 473;
Best Local Similarity 22.8%; Pred. No. 0.36;
RESULT 763
ID ABB89477 standard; protein; 118 AA.
DE Human polypeptide SEQ ID NO 1853.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 91.5; DB 5; Length 118;
Best Local Similarity 28.0%; Pred. No. 0.069;
RESULT 764
ID ADC94520 standard; protein; 291 AA.
DE E. faecium protein sequence SEQ ID 4147.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.6%; Score 91.5; DB 7; Length 291;
Best Local Similarity 22.9%; Pred. No. 0.24;
RESULT 765
ID ADN23444 standard; protein; 373 AA.
DE Bacterial polypeptide #6097.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOX/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.6%; Score 91.5; DB 8; Length 373;
Best Local Similarity 23.0%; Pred. No. 0.34;
RESULT 766
ID AAU03808 standard; protein; 387 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #7.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.6%; Score 91.5; DB 4; Length 387;
Best Local Similarity 23.0%; Pred. No. 0.35;
RESULT 767
ID ABB91939 standard; protein; 712 AA.
DE Herbicidally active polypeptide SEQ ID NO 1150.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.6%; Score 91.5; DB 5; Length 712;

Best Local Similarity 22.2%; Pred. No. 0.82;
RESULT 768
ID ADN46339 standard; protein; 451 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID217.
PN W02004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.5%; Score 90.5; DB 8; Length 451;
Best Local Similarity 21.2%; Pred. No. 0.57;
RESULT 769
ID AAB76803 standard; protein; 283 AA.
DE Corynebacterium glutamicum MCT protein SEQ ID NO:588.
PN W0200100805-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.5%; Score 90; DB 4; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.34;
RESULT 770
ID AAG89779 standard; protein; 283 AA.
DE C glutamicum protein fragment SEQ ID NO: 3533.
PN EF1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.5%; Score 90; DB 4; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.34;
RESULT 771
ID ADP98865 standard; protein; 505 AA.
DE C. albicans specific gene, orf6.4442, protein sequence.
PN W02004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 6.5%; Score 90; DB 8; Length 505;
Best Local Similarity 20.5%; Pred. No. 0.75;
RESULT 772
ID ABU45537 standard; protein; 458 AA.
DE Protein encoded by Prokaryotic essential gene #31064.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89.5; DB 6; Length 458;
Best Local Similarity 22.8%; Pred. No. 0.75;
RESULT 773
ID ABP26393 standard; protein; 579 AA.
DE Streptococcus polypeptide SEQ ID NO 1962.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.4%; Score 89.5; DB 5; Length 579;
Best Local Similarity 24.8%; Pred. No. 1;
RESULT 774
ID ABU50406 standard; protein; 428 AA.
DE Protein encoded by Prokaryotic essential gene #35933.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89; DB 6; Length 428;
Best Local Similarity 21.6%; Pred. No. 0.78;
RESULT 775
ID AAB94689 standard; protein; 637 AA.
DE Human protein sequence SEQ ID NO:15654.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 89; DB 4; Length 637;
Best Local Similarity 21.5%; Pred. No. 1.3;
RESULT 776
ID ASU23408 standard; protein; 642 AA.
DE Protein encoded by Prokaryotic essential gene #8935.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 6.4%; Score 89; DB 6; Length 642;
Best Local Similarity 20.8%; Pred. No. 1.4;
RESULT 777
ID AAU03497 standard; protein; 757 AA.
DE Human sterol sensing domain protein.
PN W0200146227-A2.
PD 28-JUN-2001.
PA (UYZU-) UNIV ZURICH.
Query Match 6.4%; Score 89; DB 4; Length 757;
Best Local Similarity 21.5%; Pred. No. 1.7;
RESULT 778
ID AAB41293 standard; protein; 758 AA.
DE Human ORF1057 polypeptide sequence SEQ ID NO:2114.
PN W0200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 89; DB 3; Length 758;
Best Local Similarity 21.5%; Pred. No. 1.7;
RESULT 779
ID AAU74820 standard; protein; 1124 AA.
DE Human REPTR 3 protein.
PN W0200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 89; DB 5; Length 1124;
Best Local Similarity 21.5%; Pred. No. 2.9;
RESULT 780
ID ADA55083 standard; protein; 1203 AA.
DE Human protein, SEQ ID 2651.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 89; DB 6; Length 1203;
Best Local Similarity 21.5%; Pred. No. 3.2;
RESULT 781
ID ABG31547 standard; protein; 1330 AA.
DE Human patched-like protein.
PN W0200246402-A2.
PD 13-JUN-2002.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 89; DB 5; Length 1330;
Best Local Similarity 21.5%; Pred. No. 3.7;
RESULT 782
ID AAB96747 standard; protein; 430 AA.
DE Putative P. abyssi permease #26.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 6.4%; Score 88.5; DB 4; Length 430;
Best Local Similarity 23.8%; Pred. No. 0.89;
RESULT 783
ID AAR37309 standard; protein; 1165 AA.
DE DE Cardiac adenylyl cyclase.
PN EP543137-A1.
PD 26-MAY-1993.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 6.3%; Score 88; DB 2; Length 1165;
Best Local Similarity 20.5%; Pred. No. 4;
RESULT 784
ID ABU19097 standard; protein; 233 AA.
DE Protein encoded by Prokaryotic essential gene #4624.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 87.5; DB 6; Length 233;
Best Local Similarity 22.8%; Pred. No. 0.5;
RESULT 785
ID ADD67113 standard; protein; 322 AA.
DE Homogentisate prenyl transferase.
PN W02003080647-A2.
PD 02-OCT-2003.

PA (MONSANTO TECHNOLOGY LLC.
Query Match 6.2%; Score 87.5; DB 7; Length 322;
Best Local Similarity 22.6%; Pred. No. 0.78;
RESULT 786
ID ADC77581 standard; protein; 453 AA.
DE Mouse TMS2 amino acid sequence.
PN W02003066829-A2.
PD 14-AUG-2003.
PA (DISCOVERY GENOMICS INC.
Query Match 6.3%; Score 87.5; DB 7; Length 453;
Best Local Similarity 19.9%; Pred. No. 1.2;
RESULT 787
ID ADS28619 standard; protein; 482 AA.
DE Bacterial polypeptide #17652.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 87.5; DB 8; Length 482;
Best Local Similarity 21.2%; Pred. No. 1.4;
RESULT 788
ID ABU33543 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #19070.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86.5; DB 6; Length 239;
Best Local Similarity 20.4%; Pred. No. 0.67;
RESULT 789
ID ADT05661 standard; protein; 261 AA.
DE Haemophilus influenzae (NTHi) protein - SEQ ID 697.
PN W02004078949-A2.
PD 16-SEP-2004.
PA (CHIL-) CHILDRENS HOSPITAL INC.
Query Match 6.2%; Score 86.5; DB 8; Length 261;
Best Local Similarity 24.2%; Pred. No. 0.76;
RESULT 790
ID ADH87029 standard; protein; 356 AA.
DE Enterococcus faecalis polypeptide #1509.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.2%; Score 86.5; DB 7; Length 356;
Best Local Similarity 19.2%; Pred. No. 1.2;
RESULT 791
ID ADS46642 standard; protein; 400 AA.
DE Bacterial polypeptide #23072.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 86.5; DB 8; Length 400;
Best Local Similarity 21.9%; Pred. No. 1.4;
RESULT 792
ID ABB47717 standard; protein; 583 AA.
DE Listeria monocytogenes protein #421.
PN W0200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.2%; Score 86.5; DB 5; Length 583;
Best Local Similarity 19.4%; Pred. No. 2.3;
RESULT 793
ID AAG39112 standard; protein; 1346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48347.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 6.2%; Score 86.5; DB 3; Length 1346;
Best Local Similarity 18.2%; Pred. No. 7.3;
RESULT 794
ID AAG39111 standard; protein; 1390 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48346.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1390;
Best Local Similarity 18.2%; Pred. No. 7.6;
RESULT 795
ID AAG39110 standard; protein; 1403 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48345.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1403;
Best Local Similarity 18.2%; Pred. No. 7.7;
RESULT 796
ID AEM73219 standard; protein; 372 AA.
DE Staphylococcus aureus protein #2459.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%; Score 86; DB 6; Length 372;
Best Local Similarity 18.1%; Pred. No. 1.4;
RESULT 797
ID AAG98347 standard; protein; 396 AA.
DE Escherichia coli protein sequence SEQ ID NO:395.
PN W0200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86; DB 4; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.5;
RESULT 798
ID ASU14798 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #325.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86; DB 6; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.5;
RESULT 799
ID ABB90798 standard; protein; 725 AA.
DE Herbicidally active polypeptide SEQ ID NO 9.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.2%; Score 86; DB 5; Length 725;
Best Local Similarity 18.9%; Pred. No. 3.5;
RESULT 800
ID AAB11039 standard; protein; 841 AA.
DE S. xylosum mprf protein.
PN DE19914817-A1.
PD 05-OCT-2000.
PA (PETR-) PETRY GENMEDICS GMBH.
Query Match 6.2%; Score 86; DB 3; Length 841;
Best Local Similarity 18.3%; Pred. No. 4.3;
RESULT 801
ID ABP77912 standard; protein; 295 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 2354.
PN W0200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.1%; Score 85.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 1.2;
RESULT 802
ID ABU37235 standard; protein; 295 AA.
DE Protein encoded by Prokaryotic essential gene #22762.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 1.2;
RESULT 803

ID ABJ39122 standard; protein; 311 AA.
DE Molecule for disease detection and treatment (MDDT)-32 protein sequence.
PN WO2003052049-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.1%; Score 85.5; DB 6; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.3;
RESULT 804
ID ADC37363 standard; protein; 311 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 196.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH-) ASAH KASEI KK.
Query Match 6.1%; Score 85.5; DB 7; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.3;
RESULT 805
ID ADR58959 standard; protein; 311 AA.
DE Human Elk1 phosphorylation/Elk1 kinase activation protein - SEQ ID 62.
PN WO2004072277-A2.
PD 26-AUG-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.1%; Score 85.5; DB 8; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.3;
RESULT 806
ID AAM93524 standard; protein; 329 AA.
DE Human polypeptide, SEQ ID NO: 3257.
PN EP1130094-A2.
PD 03-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.4;
RESULT 807
ID AAB92687 standard; protein; 329 AA.
DE Human protein sequence SEQ ID NO:11071.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.4;
RESULT 808
ID ADL31224 standard; protein; 329 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3257.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 85.5; DB 8; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.4;
RESULT 809
ID ADA98171 standard; protein; 359 AA.
DE Human secreted protein sequence #12.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 810
ID ADA44024 standard; protein; 359 AA.
DE Human secreted protein SEQ ID 212.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 811
ID ADC20341 standard; protein; 359 AA.
DE Human secreted protein - amino acid sequence #17.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 812
ID ADF10683 standard; protein; 359 AA.

DE Human secreted protein #5.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 813
ID AAB75546 standard; protein; 360 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:100.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.1%; Score 85.5; DB 4; Length 360;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 814
ID AAW61371 standard; protein; 439 AA.
DE Non-adrenergic SM binding protein.
PN EP848059-A1.
PD 17-JUN-1998.
PA (VERT-) VERTIGEN.
Query Match 6.1%; Score 85.5; DB 2; Length 439;
Best Local Similarity 23.0%; Pred. No. 2;
RESULT 815
ID AAB75598 standard; protein; 530 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:152.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.1%; Score 85.5; DB 4; Length 530;
Best Local Similarity 23.0%; Pred. No. 2.6;
RESULT 816
ID AAY94910 standard; protein; 545 AA.
DE Human secreted protein clone pk366_7 protein sequence SEQ ID NO:26.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 6.1%; Score 85.5; DB 3; Length 545;
Best Local Similarity 23.0%; Pred. No. 2.7;
RESULT 817
ID AAB94667 standard; protein; 545 AA.
DE Human protein sequence SEQ ID NO:15600.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 545;
Best Local Similarity 23.0%; Pred. No. 2.7;
RESULT 818
ID AAY82460 standard; protein; 579 AA.
DE Human SM-11044-binding receptor protein SEQ ID NO:4.
PN WO200014266-A1.
PD 16-MAR-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 6.1%; Score 85.5; DB 3; Length 579;
Best Local Similarity 23.0%; Pred. No. 3;
RESULT 819
ID AAY82459 standard; protein; 582 AA.
DE Human SM-11044-binding receptor protein SEQ ID NO:2.
PN WO200014266-A1.
PD 16-MAR-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 6.1%; Score 85.5; DB 3; Length 582;
Best Local Similarity 23.0%; Pred. No. 3;
RESULT 820
ID ABB69104 standard; protein; 700 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34104.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 85.5; DB 4; Length 700;
Best Local Similarity 19.7%; Pred. No. 3.8;
RESULT 821

ID ABU34786 standard; protein; 338 AA.
DE Protein encoded by Prokaryotic essential gene #20313.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85; DB 6; Length 338;
Best Local Similarity 23.1%; Pred. No. 1.6;
RESULT 822
ID ABU36544 standard; protein; 338 AA.
DE Protein encoded by Prokaryotic essential gene #22071.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85; DB 6; Length 338;
Best Local Similarity 23.1%; Pred. No. 1.6;
RESULT 823
ID AAG90802 standard; protein; 419 AA.
DE C glutamicum protein fragment SEQ ID NO: 4556.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.1%; Score 85; DB 4; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.2;
RESULT 824
ID AAE20418 standard; protein; 419 AA.
DE Corynebacterium glutamicum CHRS protein.
PN WO200220572-A2.
PD 14-MAR-2002.
PA (DEGS) DEGUSSA AG.
Query Match 6.1%; Score 85; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.2;
RESULT 825
ID AB55143 standard; protein; 443 AA.
DE Lactococcus lactis protein ysfC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 85; DB 5; Length 443;
Best Local Similarity 24.4%; Pred. No. 2.3;
RESULT 826
ID AAU78998 standard; protein; 498 AA.
DE Mouse Rh type C gene (RHCG) protein.
PN WO200220719-A2.
PD 14-MAR-2002.
PA (NYBL-) NEW YORK BLOOD CENT INC.
Query Match 6.1%; Score 85; DB 5; Length 498;
Best Local Similarity 20.2%; Pred. No. 2.7;
RESULT 827
ID ADE56874 standard; protein; 1166 AA.
DE Rat Protein Q03343, SEQ ID NO 2729.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GSHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 85; DB 7; Length 1166;
Best Local Similarity 19.8%; Pred. No. 8.8;
RESULT 828
ID AAB02010 standard; protein; 1180 AA.
DE Type VI adenylyl cyclase.
PN US6107076-A.
PD 22-AUG-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 6.1%; Score 85; DB 3; Length 1180;
Best Local Similarity 19.8%; Pred. No. 9;
RESULT 829
ID ADH8320 standard; protein; 296 AA.
DE Enterococcus faecalis polypeptide #2800.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 84.5; DB 7; Length 296;
Best Local Similarity 25.2%; Pred. No. 1.5;

RESULT 830
ID ABM68417 standard; protein; 324 AA.
DE Photorhabdus luminescens protein sequence #1514.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 84.5; DB 6; Length 324;
Best Local Similarity 23.8%; Pred. No. 1.7;
RESULT 831
ID AAY07771 standard; protein; 356 AA.
DE Human secreted protein fragment encoded from gene 28.
PN WO9909155-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 2; Length 356;
Best Local Similarity 19.8%; Pred. No. 2;
RESULT 832
ID ABG75197 standard; protein; 408 AA.
DE Wheat homogenisate geranylgeranyl transferase.
PN WO2003082899-A2.
PD 03-OCT-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.1%; Score 84.5; DB 7; Length 408;
Best Local Similarity 25.3%; Pred. No. 2.4;
RESULT 833
ID AAG46717 standard; protein; 446 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58803.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 84.5; DB 3; Length 446;
Best Local Similarity 19.0%; Pred. No. 2.7;
RESULT 834
ID AAY95015 standard; protein; 453 AA.
DE Human secreted protein vc61_1, SEQ ID NO:70.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGEN INC.
Query Match 6.1%; Score 84.5; DB 3; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 835
ID AAG65236 standard; protein; 453 AA.
DE Protein tyrosine kinase 50.
PN CN1298944-A.
PD 13-JUN-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 836
ID AAU29065 standard; protein; 453 AA.
DE Human PRO polypeptide sequence #42.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 837
ID AAM39489 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2634.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 838
ID AAB65170 standard; protein; 453 AA.
DE Human PRO732 (UNQ396) protein sequence SEQ ID NO:73.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 839

ID ABB90299 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2675.
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 5; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 840
ID ABUS8441 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 841
ID ABUS7989 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 842
ID ABUS4304 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 843
ID ABR66178 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 844
ID ABR65568 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 845
ID ABUS9508 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 846
ID ABUS7985 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 847
ID ABUS9063 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO732.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 848
ID ABUS2575 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 849
ID ABUS2747 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 850
ID ABUS9868 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 851
ID ABR68117 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 852
ID ABUS60494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 853
ID ABUS96170 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 854
ID ABUS92601 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 855
ID ABO08678 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 856
ID ABO02730 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 857
ID ABR74884 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 858
ID ABR94646 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 859
ID ABUS13876 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002103125-A1.

PD 01-AUG-2002.
PA (GETH) GENENTECH LTD. 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 860
ID ABU85619 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 861
ID ABU98779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 862
ID ABU97994 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 863
ID ABU91700 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 864
ID ABU89393 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 865
ID ABU86234 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 866
ID ABU67447 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 867
ID ABU80475 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 868
ID ABU72461 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 869

ID ABR99393 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 870
ID ABR98783 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 871
ID ABO16306 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 872
ID ABR92206 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 873
ID ABO18847 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 874
ID ABR78268 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 875
ID ABU85004 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 876
ID ABO00143 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 877
ID ABO11475 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 878
ID ABO02120 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 879
ID ABU88694 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.


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Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 900
ID ABR69337 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 901
ID ABO01478 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 902
ID ABO81280 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 903
ID ABR60077 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 904
ID ABR67812 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 905
ID ABR65200 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 906
ID ABR68422 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 907
ID ABR71834 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 908
ID ABUS9210 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 909
ID ABUS5314 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 910
ID ABUS9004 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 911
ID ABUS3084 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 912
ID ABUS9490 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 913
ID ABUS90488 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 914
ID ABUS3999 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 915
ID ABUS3650 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 916
ID ABO25907 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 917
ID ABR64895 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 918
ID ABR68727 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
RESULT 919
ID ABO06543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 920
ID ABO06543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
Pred. No. 2.7;
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ID ABR99088 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 921
ID ABUS6972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 922
ID ABUS924 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 923
ID ABUS2211 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 924
ID ABUS7222 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 925
ID ABUS3694 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 926
ID ABO08068 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 927
ID ABUS1779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 928
ID ABUS943 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 929
ID ABR59772 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 930
ID ABUS93960 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036155-A1.
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PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 931
ID ABUS9813 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 932
ID ABR66483 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 933
ID ABR90901 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 934
ID ABUS8916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 935
ID ABUS4328 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 936
ID ABUS79210 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 937
ID ABUS6539 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 938
ID ABUS6844 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 939
ID ABUS4633 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 940
ID ABO04560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032107-A1.
PD 13-FEB-2003.
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Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 941
ID ABR70309 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 942
ID ABU92294 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 943
ID ABU98474 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 944
ID ABR65873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 945
ID ABR64590 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 946
ID ABU93959 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO1120.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 947
ID ABU79515 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 948
ID ABU92906 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 949
ID ABU95865 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 950
ID ABU91085 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 951
ID ABR90178 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 952
ID ABO09593 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 953
ID ABO10865 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 954
ID ABR70919 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 955
ID ABU87527 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 956
ID ABR91395 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 957
ID ABR84609 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 958
ID ABR69699 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 959
ID ABU80076 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 960
ID ABU92125 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 961
ID ABR93345 standard; protein; 453 AA.
DE Human PRO polypeptide #42.

RESULT 951
ID ABR90178 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 952
ID ABO09593 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 953
ID ABO10865 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 954
ID ABR70919 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 955
ID ABU87527 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 956
ID ABR91395 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 957
ID ABR84609 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 958
ID ABR69699 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 959
ID ABU80076 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 960
ID ABU92125 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 961
ID ABR93345 standard; protein; 453 AA.
DE Human PRO polypeptide #42.

PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 962
ID ABO0898 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 963
ID ABO08983 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 964
ID ABU10831 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 965
ID ABU10551 standard; protein; 453 AA.
DE Human secreted/transmembrane protein #42.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 966
ID ABU1583 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 967
ID ABU95560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 968
ID ABU96769 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 969
ID ABR70614 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 970
ID ABO04965 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 971
ID ABO08373 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 972
ID ABU8522 standard; protein; 453 AA.
DE Human secreted and transmembrane polypeptide PRO732.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 973
ID ABO34036 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 974
ID ABO05580 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 975
ID ABR73969 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 976
ID ABR95561 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 977
ID ABR80858 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 978
ID ABR81163 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 979
ID ABM00859 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 980
ID ABR88461 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003086743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1000
ID ABM06098 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1001
ID ABM03604 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1002
ID ABM35055 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1003
ID ABM26292 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1004
ID ABO48074 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1005
ID ABR92816 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1006
ID ABO24577 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1007
ID ADA37584 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1008
ID ABM1588 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1009
ID ABM02689 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1010
ID ABM15985 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1011
ID ABO27546 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003084451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1012
ID ABM29037 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1013
ID ABM07013 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1014
ID ABM21107 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003088707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1015
ID ABM09453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1016
ID ABO41323 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1017
ID ABO36138 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1018
ID ABO43667 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1019
ID ABM76367 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1020
ID ABM76063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1021
ID ABM25682 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1022
ID ABM25987 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1023
ID ADA21270 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1024
ID ABO03340 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1025
ID ABO02425 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1026
ID ABR90596 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1027
ID ABR73664 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1028
ID ABO16916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1029
ID ABR94341 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1030
ID ABR75848 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1031
ID ABR71224 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1032
ID ABR93121 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1033
ID ABR93426 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1034
ID ADA10057 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1035
ID ABR87851 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1036
ID ABO27851 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1037
ID ABO29986 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1038
ID ABO33195 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1039
ID ABM04883 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1040
ID ABM08843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1041
ID ABO36443 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1042
ID ABO35528 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1043
ID ABO39493 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1044
ID ABM10368 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1045
ID ABM1893 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1046
ID ABO52039 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049768-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1047
ID ABO52344 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1048
ID ABO23662 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1049
ID ADA17601 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1050
ID ABR97148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1051
ID ABR86936 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1052
ID ABM10978 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1053
ID ABM28122 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1054
ID ABO32121 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1055
ID ABM15248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

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Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1075
ID ABO20802 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1076
ID ABO41933 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1077
ID ABO42543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1078
ID ABO10063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1079
ID ABO38578 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1080
ID ABO32818 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1081
ID ABO22632 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1082
ID ABO74843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1083
ID ADA79628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1084
ID ABR96233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068742-A1.
PD 10-APR-2003.

PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1085
ID ABO2384 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1086
ID ABR86326 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1087
ID ABR86631 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1088
ID ABM16595 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1089
ID ABM29647 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1090
ID ABO29071 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1091
ID ABM23852 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1092
ID ABM23242 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1093
ID ABM22022 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068742-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1094
 ID ABO37663 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068756-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1095
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003082715-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1096
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003082715-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1097
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003082715-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1098
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003082715-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1099
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003096359-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1100
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003100061-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1101
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003032125-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1102
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054454-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1103
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068756-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054477-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1104
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054460-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1105
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003059832-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1106
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049753-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1107
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049763-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1108
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073172-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1109
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073172-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1110
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068700-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1111
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003088736-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1112
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068756-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1113
ID ABO38273 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1114
ID ABO45573 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1115
ID ABR20497 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1116
ID ADA81355 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1117
ID ABO16611 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1118
ID ABO18237 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1119
ID ABO22664 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1120
ID ABO22969 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1121
ID ABR92511 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1122
ID ABR81468 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1123
ID ABO77892 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1124
ID ABR9681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1125
ID ABO26597 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1126
ID ABO13723 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1127
ID ABO28461 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1128
ID ABO30291 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1129
ID ABO7318 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1130
ID ABO3909 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1131
ID ABO37053 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068719-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1132	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO41628 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003068729-A1.	PD 10-APR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1133	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO35223 standard; protein; 453 AA.	DE Human PRO polypeptide #42.	PN US2003068738-A1.	PD 10-APR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1134	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO25072 standard; protein; 453 AA.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.	PN US2003104540-A1.	PD 05-JUN-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1135	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO47464 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003049742-A1.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1136	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO47769 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003049747-A1.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1137	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO48379 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003049750-A1.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1138	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO51429 standard; protein; 453 AA.	DE Human PRO polypeptide #42.	PN US2003049766-A1.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1139	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO51734 standard; protein; 453 AA.	DE Human PRO polypeptide #42.	PN US2003049767-A1.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1140	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO50514 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003049779-A1.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1141	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABR79638 standard; protein; 453 AA.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.	PN US2003040059-A1.	PD 27-FEB-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1142	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO16900 standard; protein; 453 AA.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.	PN US2003040078-A1.	PD 27-FEB-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1143	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO17932 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003044918-A1.	PD 06-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1144	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO20884 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003032132-A1.	PD 13-FEB-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1145	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABR96843 standard; protein; 453 AA.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.	PN US2003054462-A1.	PD 20-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1146	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ADA38514 standard; protein; 453 AA.	DE Human secreted/transmembrane protein PRO732.	PN US2003059780-A1.	PD 27-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1147	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO12198 standard; protein; 453 AA.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.	PN US2003064445-A1.	PD 03-APR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1148	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO16290 standard; protein; 453 AA.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.	PN US2003064449-A1.	PD 03-APR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1149	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO24157 standard; protein; 453 AA.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.	PN US2003064441-A1.	PD 03-APR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1150	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO14638 standard; protein; 453 AA.	DE Human secreted polypeptide PRO732, SEQ ID NO:84.	PN US2003068696-A1.	PD 10-APR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1151	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO50514 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003049779-A1.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1152	Best Local Similarity	19.8%; Pred. No. 2.7;	
ID ABO50514 standard; protein; 453 AA.	DE Human secreted/transmembrane protein (PRO) #42.	PN US2003049779-A1.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	Query Match	Best Local Similarity	6.1%; Score 84.5; DB 6; Length 453;
RESULT 1153	Best Local Similar		

RESULT 1170
ID ABO20579 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1171
ID ABO25322 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1172
ID ABO25627 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1173
ID ABR94036 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1174
ID ADA92635 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1175
ID ABR79943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1176
ID ABM11283 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1177
ID ABO32890 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1178
ID ABO30596 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1179
ID ABO30901 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064468-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1180
ID ABO27207 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1181
ID ABM29952 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003088769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1182
ID ABM05488 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1183
ID ABM15553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1184
ID ABM08538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003088759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1185
ID ABO42238 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1186
ID ABO37968 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1187
ID ABO45878 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1188
ID ABM66681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068688-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1189
ID ABO49904 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1190
ID ABO50819 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1191
ID ABO49294 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1192
ID ABO49599 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1193
ID ADA78448 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1194
ID ABR88156 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1195
ID ABM26902 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1196
ID ABM03299 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1197
ID ABO39798 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1198
ID ABO49904 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1199
ID ABO50819 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1200
ID ABO5275 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1201
ID ABR74579 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1202
ID ABR77058 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1203
ID ABM17815 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1204
ID ABR95866 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1205
ID ABO21799 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1206
ID ABO19969 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1207
ID ABO24272 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003084467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 1217	ID ABM19277 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	
FN US2003104551-A1.	
PD 05-JUN-2003.	
PA (GETH) GENENTECH INC.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1218	ID ABO46488 standard; protein; 453 AA.
DE Human PRO polypeptide #42.	
FN US2003049761-A1.	
PD 13-MAR-2003.	
PA (GETH) GENENTECH INC.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1219	ID ABO48989 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.	
FN US2003049757-A1.	
PD 13-MAR-2003.	
PA (GETH) GENENTECH INC.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1220	ID ABR69032 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	
FN US2003027273-A1.	
PD 06-FEB-2003.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1221	ID ABR89071 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	
FN US2003036119-A1.	
PD 20-FEB-2003.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1222	ID ABR72444 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	
FN US2003036120-A1.	
PD 20-FEB-2003.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1223	ID ABR74274 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	
FN US2003036161-A1.	
PD 20-FEB-2003.	
PA (GETH) GENENTECH INC.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1224	ID ABO18542 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.	
FN US2003044921-A1.	
PD 06-MAR-2003.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1225	ID ABR80248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	
FN US2003049739-A1.	
PD 13-MAR-2003.	
PA (GETH) GENENTECH INC.	
Query Match	6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity	19.8%; Pred. No. 2.7;
RESULT 1226	ID ABRN01469 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.	
FN US2003059882-A1.	
PD 27-MAR-2003.	

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1227
ID ABM02079 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1228
ID ABR87241 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1229
ID ABM12808 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1230
ID ABM30562 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1231
ID ABM24462 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1232
ID ABO29376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1233
ID ABO31206 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1234
ID ABM14333 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1235
ID ABM09758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1236
ID ABO38883 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1237
ID ABM34648 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1238
ID ABO51124 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1239
ID ABO03950 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1240
ID ABO10420 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1241
ID ABO53122 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1242
ID ABR77663 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1243
ID ABR78873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1244
ID ABO23967 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1245
ID ABR93731 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054457-A1.
PD 20-MAR-2003.

RESULT 1255

ID ABO40103 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068681-A1.
PD 10-APR-2003.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1256

ID ABM74538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096351-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1257

ID ABW33733 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096358-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1258

ID ABW20192 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104556-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1259

ID ABO48684 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049756-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1260

ID ABO22492 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003017982-A1.
PD 23-JAN-2003.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1261

ID ABR72749 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036122-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1262

ID ABO15391 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036121-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1263

ID ABR85106 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040065-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
Result 19.8%; Pred. No. 2.7;

RESULT 1264

ID ABO15086 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044919-A1.
PD 06-MAR-2003.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1265
ID ABO17221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1266
ID ABM17510 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1267
ID ADA06362 standard; protein; 453 AA.
DE Human secreted/transmembrane PRO polypeptide #17.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1268
ID ADA39055 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1269
ID ABR85411 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1270
ID ABM76977 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1271
ID ABO28156 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1272
ID ABM22937 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1273
ID ABM30257 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1274
ID ABM21717 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1275
ID ABM21412 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1276
ID ABM14943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1277
ID ABO41018 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1278
ID ABO36748 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1279
ID ABO37358 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1280
ID ABM75148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1281
ID ABM33428 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1282
ID ABO46183 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1283
ID ADA82519 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049755-A1.


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PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1284
ID ADB96081 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1285
ID ABM311782 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1286
ID ABM31172 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1287
ID ADB85827 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1288
ID ABM32087 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1289
ID ABM32392 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1290
ID ABM31477 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1291
ID ABM30867 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1292
ID ADC57553 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1293
ID ADC54917 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1294
ID ADC11784 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1295
ID ADC56206 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1296
ID ADC07261 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1297
ID ADC11251 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1298
ID ADC14373 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1299
ID ADD07905 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1300
ID ADC81730 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1301
ID ADD07372 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1302
ID ADC77580 standard; protein; 453 AA.
DE Human TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1303
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ID ADC82263 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1304
ID ADD05557 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1305
ID ADD08443 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1306
ID ADD06692 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1307
ID ADC82939 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1308
ID ADD55046 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1309
ID ADD56004 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1310
ID ADD54442 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1311
ID ADE26596 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1312
ID ABE26063 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1313

ID ADF67000 standard; protein; 453 AA.
DE Human PRO732 amino acid sequence SEQ ID NO:73.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1314
ID ADG02552 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US20030207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1315
ID ADG01259 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US20030207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1316
ID ADF95434 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US20030207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1317
ID ADG12249 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US20030207392-A1.
PD 06-NOV-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1318
ID ADH08909 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US20030207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1319
ID ADI35254 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1320
ID ADH99746 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1321
ID ADL32690 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US20030207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1322
ID ADM30224 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073813-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 7; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1323
 ID ADE74221 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003211572-A1.
 PD 13-NOV-2003.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1324
 ID ADE74833 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003211574-A1.
 PD 13-NOV-2003.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1325
 ID ADF35199 standard; protein; 453 AA.
 DE Human PRO732 polypeptide.
 PN US2003194760-A1.
 PD 16-OCT-2003.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1326
 ID ADG11449 standard; protein; 453 AA.
 DE Human PRO732 polypeptide.
 PN US2003228655-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1327
 ID ADF96046 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215909-A1.
 PD 20-NOV-2003.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1328
 ID ADG04317 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215912-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1329
 ID ADG00477 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215911-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1330
 ID ADG82733 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003215910-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1331
 ID ADH26014 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003068770-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1332
 ID ADH19319 standard; protein; 453 AA.

DE Human secreted/transmembrane protein PRO732.
 PN US2003228656-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1333
 ID ADH32983 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003068768-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1334
 ID ADH20812 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003224358-A1.
 PD 04-DEC-2003.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1335
 ID ADH19852 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003219856-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1336
 ID ADJ54722 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2004023321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1337
 ID ADJ64493 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2004038337-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1338
 ID ADM31389 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004048334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1339
 ID ADM36436 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004053358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1340
 ID ADM40241 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 2.7;
 RESULT 1341
 ID ADN37849 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004091959-A1.

PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1342
ID ADR09184 standard; protein; 453 AA.
DE Human protein useful for treating neurological disease Seq 2690.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1343
ID A8M80816 standard; protein; 453 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81457, SEQ:2102.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1344
ID ADR99176 standard; protein; 453 AA.
DE KIAA1253, SEQ ID 182.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1345
ID ADG10618 standard; protein; 472 AA.
DE Human STAT6-activating protein, SEQ ID NO:208.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 6.1%; Score 84.5; DB 7; Length 472;
Best Local Similarity 19.8%; Pred. No. 2.9;
RESULT 1346
ID AAM41275 standard; protein; 477 AA.
DE Human polypeptide SEQ ID NO 6206.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 84.5; DB 4; Length 477;
Best Local Similarity 19.8%; Pred. No. 2.9;
RESULT 1347
ID AAG46716 standard; protein; 521 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58802.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 84.5; DB 3; Length 521;
Best Local Similarity 19.0%; Pred. No. 3.3;
RESULT 1348
ID ABB93783 standard; protein; 562 AA.
DE Herbicidally active polypeptide SEQ ID NO 2994.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 84.5; DB 5; Length 562;
Best Local Similarity 19.6%; Pred. No. 3.7;
RESULT 1349
ID AAG46715 standard; protein; 571 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58801.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 84.5; DB 3; Length 571;
Best Local Similarity 19.0%; Pred. No. 3.8;
RESULT 1350
ID ADA36714 standard; protein; 241 AA.
DE Acinetobacter baumannii protein #3875.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 6; Length 241;
Best Local Similarity 20.3%; Pred. No. 4.6;
DE Pseudomonas aeruginosa polypeptide #3010.

Best Local Similarity 22.8%; Pred. No. 1.3;
RESULT 1351
ID ABG61495 standard; protein; 318 AA.
DE Iron uptake ABC transporter polypeptide #2.
PN WO200234773-A2.
PD 02-MAY-2002.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match 6.0%; Score 84; DB 5; Length 318;
Best Local Similarity 24.4%; Pred. No. 1.9;
RESULT 1352
ID ABU02362 standard; protein; 318 AA.
DE S. pneumoniae type 4 strain protein from coding region #1940.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 84; DB 6; Length 318;
Best Local Similarity 24.4%; Pred. No. 1.9;
RESULT 1353
ID ABG10541 standard; protein; 480 AA.
DE Novel human diagnostic protein #10532.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 84; DB 4; Length 480;
Best Local Similarity 20.5%; Pred. No. 3.4;
RESULT 1354
ID ADL04919 standard; protein; 506 AA.
DE M. catarrhalis protein #685.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 8; Length 506;
Best Local Similarity 19.9%; Pred. No. 3.6;
RESULT 1355
ID ADS23392 standard; protein; 516 AA.
DE Bacterial polypeptide #12425.
PN US200233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.0%; Score 84; DB 8; Length 516;
Best Local Similarity 25.0%; Pred. No. 3.7;
RESULT 1356
ID ABO67632 standard; protein; 537 AA.
DE Klebsiella pneumoniae polypeptide seqid 14149.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 537;
Best Local Similarity 18.7%; Pred. No. 3.9;
RESULT 1357
ID ABU38257 standard; protein; 575 AA.
DE Protein encoded by Prokaryotic essential gene #23784.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 84; DB 6; Length 575;
Best Local Similarity 20.3%; Pred. No. 4.3;
RESULT 1358
ID ABO73781 standard; protein; 602 AA.
DE Pseudomonas aeruginosa polypeptide #5956.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 602;
Best Local Similarity 20.3%; Pred. No. 4.6;
RESULT 1359
ID ABO70835 standard; protein; 720 AA.
DE Pseudomonas aeruginosa polypeptide #3010.

PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 720;
Best Local Similarity 21.8%; Pred. No. 5.9;
RESULT 1360
ID ABU32051 standard; protein; 1137 AA.
DE Protein encoded by Prokaryotic essential gene #17578.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 84; DB 6; Length 1137;
Best Local Similarity 18.6%; Pred. No. 11;
RESULT 1361
ID ABO67057 standard; protein; 1138 AA.
DE Klebsiella pneumoniae polypeptide seqid 13574.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 1138;
Best Local Similarity 18.6%; Pred. No. 11;
RESULT 1362
ID ABU37874 standard; protein; 295 AA.
DE Protein encoded by Prokaryotic essential gene #23401.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 2;
RESULT 1363
ID AAR97984 standard; protein; 618 AA.
DE DmORF1 potassium channel protein.
PN WO9613520-A1.
PD 09-MAY-1996.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 6.0%; Score 83.5; DB 2; Length 618;
Best Local Similarity 19.9%; Pred. No. 5.4;
RESULT 1364
ID AAU07616 standard; protein; 618 AA.
DE Drosophila melanogaster potassium ion channel ORF1 (DmORF1) protein.
PN WO200161006-A2.
PD 23-AUG-2001.
PA (BADI) BASF CORP.
Query Match 6.0%; Score 83.5; DB 4; Length 618;
Best Local Similarity 19.9%; Pred. No. 5.4;
RESULT 1365
ID ABG30123 standard; protein; 1027 AA.
DE Novel human diagnostic protein #30114.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 83.5; DB 4; Length 1027;
Best Local Similarity 19.8%; Pred. No. 11;
RESULT 1366
ID ABU28293 standard; protein; 1090 AA.
DE Protein encoded by Prokaryotic essential gene #13820.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83.5; DB 6; Length 1090;
Best Local Similarity 18.5%; Pred. No. 12;
RESULT 1367
ID AAG44538 standard; protein; 250 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55802.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 3; Length 250;
Best Local Similarity 21.7%; Pred. No. 1.8;
RESULT 1368
ID AAG66371 standard; protein; 305 AA.
DE Human olfactory receptor-like protein OLF3 #2.
PN WO200155179-A2.
PD 02-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 83; DB 4; Length 305;
Best Local Similarity 20.6%; Pred. No. 2.3;
RESULT 1369
ID AAY85935 standard; protein; 318 AA.
DE S. pneumoniae derived protein #144.
PN WO9806734-A1.
PD 19-FEB-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 6.0%; Score 83; DB 2; Length 318;
Best Local Similarity 24.4%; Pred. No. 2.5;
RESULT 1370
ID ADK46461 standard; protein; 318 AA.
DE Streptococcus pneumoniae protein, Seq ID No 2976.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 8; Length 318;
Best Local Similarity 24.4%; Pred. No. 2.5;
RESULT 1371
ID AAG71916 standard; protein; 319 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1597.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (VEDA) YEDA RES & DEV CO LTD.
Query Match 6.0%; Score 83; DB 4; Length 319;
Best Local Similarity 20.8%; Pred. No. 2.5;
RESULT 1372
ID AAB46999 standard; protein; 321 AA.
DE Human OLFXY protein.
PN DE19937839-A1.
PD 15-FEB-2001.
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
Query Match 6.0%; Score 83; DB 4; Length 321;
Best Local Similarity 20.6%; Pred. No. 2.5;
RESULT 1373
ID ABP95927 standard; protein; 321 AA.
DE Human GPCR polypeptide SEQ ID NO 664.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.0%; Score 83; DB 5; Length 321;
Best Local Similarity 20.6%; Pred. No. 2.5;
RESULT 1374
ID ADR96441 standard; protein; 336 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 5076.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 8; Length 336;
Best Local Similarity 24.4%; Pred. No. 2.7;
RESULT 1375
ID ABU43979 standard; protein; 355 AA.
DE Protein encoded by Prokaryotic essential gene #29506.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83; DB 6; Length 355;
Best Local Similarity 23.0%; Pred. No. 2.9;
RESULT 1376
ID ASO62213 standard; protein; 417 AA.
DE Klebsiella pneumoniae polypeptide seqid 8730.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 7; Length 417;
Best Local Similarity 20.8%; Pred. No. 3.6;
RESULT 1377
ID AAY66647 standard; protein; 455 AA.
DE Membrane-bound protein PRO732.
PN WO9963088-A2.

PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 83; DB 3; Length 455;
Best Local Similarity 19.8%; Pred. No. 4.1;
RESULT 1378
ID AAB96670 standard; protein; 490 AA.
DE Putative P. abyssi succinyl-CoA synthetase #5.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 6.0%; Score 83; DB 4; Length 490;
Best Local Similarity 23.6%; Pred. No. 4.5;
RESULT 1379
ID ABO70524 standard; protein; 542 AA.
DE Pseudomonas aeruginosa polypeptide #2699.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 7; Length 542;
Best Local Similarity 20.2%; Pred. No. 5.2;
RESULT 1380
ID ADA33498 standard; protein; 632 AA.
DE Acinetobacter baumannii protein #659.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 6; Length 632;
Best Local Similarity 25.1%; Pred. No. 6.4;
RESULT 1381
ID ABB65640 standard; protein; 774 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23712.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 83; DB 4; Length 774;
Best Local Similarity 22.4%; Pred. No. 8.5;
RESULT 1382
ID AUJ38963 standard; protein; 774 AA.
DE Drosophila G-protein coupled receptor, GCPR #41.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 83; DB 4; Length 774;
Best Local Similarity 22.4%; Pred. No. 8.5;
RESULT 1383
ID ADC35871 standard; protein; 774 AA.
DE Drosophila G protein coupled receptor seq id 43.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 83; DB 7; Length 774;
Best Local Similarity 22.4%; Pred. No. 8.5;
RESULT 1384
ID AAE38199 standard; protein; 802 AA.
DE Fruit fly G protein-coupled receptor (GPCR) protein #48.
PN WO2003052078-A2.
PD 26-JUN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.0%; Score 83; DB 7; Length 802;
Best Local Similarity 22.4%; Pred. No. 8.9;
RESULT 1385
ID ABP70924 standard; protein; 2159 AA.
DE Maize DEK1 from B73.
PN WO2003011015-A2.
PD 13-FEB-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 6.0%; Score 83; DB 6; Length 2159;
Best Local Similarity 20.6%; Pred. No. 35;
RESULT 1386
ID ADS43623 standard; protein; 391 AA.
DE Bacterial polypeptide #22053.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82.5; DB 8; Length 391;
Best Local Similarity 23.2%; Pred. No. 3.8;
RESULT 1387
ID ABU28011 standard; protein; 395 AA.
DE Protein encoded by Prokaryotic essential gene #13538.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 82.5; DB 6; Length 395;
Best Local Similarity 19.7%; Pred. No. 3.8;
RESULT 1388
ID AAW21009 standard; protein; 461 AA.
DE H. pylori cell envelope transporter protein, hp5ell1726orf7.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 5.9%; Score 82.5; DB 2; Length 461;
Best Local Similarity 21.5%; Pred. No. 4.7;
RESULT 1389
ID ABO69393 standard; protein; 492 AA.
DE Pseudomonas aeruginosa polypeptide #1568.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 82.5; DB 7; Length 492;
Best Local Similarity 19.1%; Pred. No. 5.2;
RESULT 1390
ID ADN18812 standard; protein; 596 AA.
DE Bacterial polypeptide #1465.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82.5; DB 8; Length 596;
Best Local Similarity 20.6%; Pred. No. 6.7;
RESULT 1391
ID ABG06558 standard; protein; 875 AA.
DE Novel human diagnostic protein #6549.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 82.5; DB 4; Length 875;
Best Local Similarity 26.0%; Pred. No. 11;
RESULT 1392
ID ADJ69204 standard; protein; 1457 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1010.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.9%; Score 82.5; DB 7; Length 1457;
Best Local Similarity 26.0%; Pred. No. 23;
RESULT 1393
ID ADJ69205 standard; protein; 1457 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1011.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.9%; Score 82.5; DB 7; Length 1457;
Best Local Similarity 26.0%; Pred. No. 23;
RESULT 1394
ID ADJ58460 standard; protein; 1457 AA.
DE BAB13458.1(P450G5) protein.

PN WO2004011648-A2.
PD 05-FEB-2004.
PA (INPH-) INFARMATICA LTD.
Query Match Similarity 5.9%; Score 82.5; DB 8; Length 1457;
Best Local Similarity 26.0%; Pred. No. 23;
RESULT 1395
ID ADC31246 standard; protein; 2548 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1328.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.9%; Score 82.5; DB 7; Length 2548;
Best Local Similarity 26.0%; Pred. No. 50;
RESULT 1396
ID AB084919 standard; protein; 219 AA.
DE Human cancer-associated protein (CAP) HP07-069.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 5.9%; Score 82; DB 8; Length 219;
Best Local Similarity 22.1%; Pred. No. 1.9;
RESULT 1397
ID AAB87783 standard; protein; 299 AA.
DE Rat T2R3 amino acid sequence SEQ ID NO:81.
PN WO200118050-A2.
PD 15-MAR-2001.
PA (REGC-) UNIV CALIFORNIA.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 5.9%; Score 82; DB 4; Length 299;
Best Local Similarity 22.8%; Pred. No. 3;
RESULT 1398
ID ADJ84452 standard; protein; 299 AA.
DE Rat T2R G-protein coupled receptor seq id 5.
PN US2004038312-A1.
PD 26-FEB-2004.
PA (ZUKE/) ZUKER C S.
PA (ADLE/) ADLER J E.
PA (HOON/) HOON M.
PA (RYBA/) RYBA N.
PA (MUEL/) MUELLER K.
Query Match
Best Local Similarity 5.9%; Score 82; DB 8; Length 299;
Best Local Similarity 22.8%; Pred. No. 3;
RESULT 1399
ID ADR29142 standard; protein; 299 AA.
DE Taste receptor modulation-related rat T2R3 protein sequence SeqID81.
PN WO2004069191-A2.
PD 19-AUG-2004.
PA (SENO-) SENOMYX INC.
Query Match
Best Local Similarity 5.9%; Score 82; DB 8; Length 299;
Best Local Similarity 22.8%; Pred. No. 3;
RESULT 1400
ID AAB10684 standard; protein; 356 AA.
DE A. thaliana PUP1 protein.
PN DE19907209-A1.
PD 24-AUG-2000.
PA (FROM/) FROMMER W.
Query Match
Best Local Similarity 5.9%; Score 82; DB 3; Length 356;
Best Local Similarity 19.4%; Pred. No. 3.8;
RESULT 1401
ID ABB91157 standard; protein; 356 AA.
DE Herbicidally active polypeptide SEQ ID NO 368.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB-) BAYER AG.
Query Match
Best Local Similarity 5.9%; Score 82; DB 5; Length 356;
Best Local Similarity 19.4%; Pred. No. 3.8;
RESULT 1402
ID ABU28157 standard; protein; 417 AA.
DE Protein encoded by Prokaryotic essential gene #13684.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 5.9%; Score 82; DB 6; Length 417;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1403
ID ADK16901 standard; protein; 465 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #426.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match
Best Local Similarity 5.9%; Score 82; DB 8; Length 465;
Best Local Similarity 23.7%; Pred. No. 5.5;
RESULT 1404
ID AB081608 standard; protein; 474 AA.
DE Pseudomonas aeruginosa polypeptide #13783.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 5.9%; Score 82; DB 7; Length 474;
Best Local Similarity 20.1%; Pred. No. 5.6;
RESULT 1405
ID ADN23219 standard; protein; 573 AA.
DE Bacterial polypeptide #5872.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 5.9%; Score 82; DB 8; Length 573;
Best Local Similarity 18.5%; Pred. No. 7.3;
RESULT 1406
ID ADN23218 standard; protein; 573 AA.
DE Bacterial polypeptide #5871.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 5.9%; Score 82; DB 8; Length 573;
Best Local Similarity 18.5%; Pred. No. 7.3;
RESULT 1407
ID ABU50193 standard; protein; 1139 AA.
DE Protein encoded by Prokaryotic essential gene #35720.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 5.9%; Score 82; DB 6; Length 1139;
Best Local Similarity 19.5%; Pred. No. 19;
RESULT 1408
ID AAE04312 standard; protein; 1167 AA.
DE Human modified cardiac adenylylase VI (ACVI) isoform.
PN WO200148164-A2.
PD 05-JUL-2001.
PA (REGC-) UNIV CALIFORNIA.
Query Match
Best Local Similarity 5.9%; Score 82; DB 4; Length 1167;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1409
ID ABG32870 standard; protein; 1167 AA.
DE Chimaeric Adenylylase isoform 6, AC-VI.
PN US2002103147-A1.
PD 01-AUG-2002.
PA (HAMM/) HAMMOND H K.
PA (INSE/) INSEL P A.
PA (PING/) PING P.
PA (POST/) POST S R.
PA (GAOM/) GAO M.
Query Match
Best Local Similarity 5.9%; Score 82; DB 5; Length 1167;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1410
ID AAW30599 standard; protein; 1168 AA.
DE Human type VI adenylyl cyclase.
PN WO9901547-A1.

PD 14-JAN-1999.
 PA (CORT-) COR THERAPEUTICS INC.
 Query Match 5.9%; Score 82; DB 2; Length 1168;
 Best Local Similarity 20.2%; Pred. No. 19;
 RESULT 1411
 ID AAB04311 standard; protein; 1168 AA.
 DE Human cardiac adenylyclase VI (ACVI) isoform #2.
 PN W0200148164-A2.
 PD 05-JUL-2001.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 5.9%; Score 82; DB 4; Length 1168;
 Best Local Similarity 20.2%; Pred. No. 19;
 RESULT 1412
 ID ABG32869 standard; protein; 1168 AA.
 DE Human Adenylylase isoform 6, AC-VI, #2.
 PN US2002103147-A1.
 PD 01-AUG-2002.
 PA (HAMM/) HAMMOND H K.
 PA (INSE/) INSEL P A.
 PA (PING/) PING P.
 PA (POST/) POST S R.
 PA (GAOM/) GAO M.
 Query Match 5.9%; Score 82; DB 5; Length 1168;
 Best Local Similarity 20.2%; Pred. No. 19;
 RESULT 1413
 ID ADE56876 standard; protein; 1168 AA.
 DE Human Protein O4306, SEQ ID NO 2731.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GSHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 5.9%; Score 82; DB 7; Length 1168;
 Best Local Similarity 20.2%; Pred. No. 19;
 RESULT 1414
 ID ADQ89850 standard; protein; 1168 AA.
 DE Antagonist of cell cycle progression polypeptide #140.
 PN W02004063362-A2.
 PD 29-JUL-2004.
 PA (CYCL-) CYCLACEL LTD.
 Query Match 5.9%; Score 82; DB 8; Length 1168;
 Best Local Similarity 20.2%; Pred. No. 19;
 RESULT 1415
 ID ADK46612 standard; protein; 199 AA.
 DE Streptococcus pneumoniae protein, Seq ID No 3127.
 PN US669703-B1.
 PD 02-MAR-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 81.5; DB 8; Length 199;
 Best Local Similarity 20.2%; Pred. No. 1.9;
 RESULT 1416
 ID ABU02196 standard; protein; 205 AA.
 DE S. pneumoniae type 4 strain protein from coding region #1774.
 PN W0200277021-A2.
 PD 03-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 5.9%; Score 81.5; DB 6; Length 205;
 Best Local Similarity 20.2%; Pred. No. 2;
 RESULT 1417
 ID AAY81546 standard; protein; 206 AA.
 DE Streptococcus pneumoniae type 4 protein sequence #46.
 PN W0200006737-A2.
 PD 10-FEB-2000.
 PA (MICR-) MICROBIAL TECHNIQS LTD.
 Query Match 5.9%; Score 81.5; DB 3; Length 206;
 Best Local Similarity 20.2%; Pred. No. 2;
 RESULT 1418
 ID ADE96056 standard; protein; 208 AA.
 DE Novel S. pneumoniae protein sequence, SEQ ID 4691.
 PN US6800744-B1.
 PD 05-OCT-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 81.5; DB 8; Length 208;

Best Local Similarity 20.2%; Pred. No. 2.1;
 RESULT 1419
 ID ABU1035 standard; protein; 278 AA.
 DE Protein encoded by Prokaryotic essential gene #26562.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 81.5; DB 6; Length 278;
 Best Local Similarity 21.0%; Pred. No. 3.1;
 RESULT 1420
 ID ADF05890 standard; protein; 280 AA.
 DE Bacterial polypeptide #2003.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 81.5; DB 7; Length 280;
 Best Local Similarity 21.0%; Pred. No. 3.1;
 RESULT 1421
 ID ABB91156 standard; protein; 351 AA.
 DE Herbicidally active polypeptide SEQ ID NO 367.
 PN W0200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 5.9%; Score 81.5; DB 5; Length 351;
 Best Local Similarity 23.1%; Pred. No. 4.2;
 RESULT 1422
 ID AAM93355 standard; protein; 399 AA.
 DE Human polypeptide, SEQ ID NO: 2909.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 5.9%; Score 81.5; DB 4; Length 399;
 Best Local Similarity 22.6%; Pred. No. 5;
 RESULT 1423
 ID ADL30876 standard; protein; 399 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 2909.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.9%; Score 81.5; DB 8; Length 399;
 Best Local Similarity 22.6%; Pred. No. 5;
 RESULT 1424
 ID ABU39717 standard; protein; 425 AA.
 DE Protein encoded by Prokaryotic essential gene #25244.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 81.5; DB 6; Length 425;
 Best Local Similarity 19.6%; Pred. No. 5.5;
 RESULT 1425
 ID AAU33707 standard; protein; 438 AA.
 DE Pseudomonas aeruginosa cellular proliferation protein #151.
 PN W0200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 81.5; DB 4; Length 438;
 Best Local Similarity 20.3%; Pred. No. 5.7;
 RESULT 1426
 ID ABU15597 standard; protein; 438 AA.
 DE Protein encoded by Prokaryotic essential gene #1124.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 81.5; DB 6; Length 438;
 Best Local Similarity 20.3%; Pred. No. 5.7;
 RESULT 1427
 ID ABO83917 standard; protein; 503 AA.
 DE Pseudomonas aeruginosa polypeptide #16092.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 81.5; DB 7; Length 503;
 Best Local Similarity 20.3%; Pred. No. 6.9;

RESULT 1428
ID ABP65039 standard; protein; 234 AA.
DE Mouse membrane spanning 4-domain family, subfamily A 7 protein.
PN WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 5.8%; Score 81; DB 5; Length 234;
Best Local Similarity 20.6%; Pred. No. 2.8;
RESULT 1429
ID ADP43824 standard; protein; 293 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 119.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 5.8%; Score 81; DB 7; Length 293;
Best Local Similarity 18.4%; Pred. No. 3.7;
RESULT 1430
ID ADA34894 standard; protein; 323 AA.
DE Acinetobacter baumannii protein #2055.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 81; DB 6; Length 323;
Best Local Similarity 22.5%; Pred. No. 4.3;
RESULT 1431
ID AAO20532 standard; protein; 392 AA.
DE Protein of the human TPM-2 gene sequence.
PN WO200229041-A2.
PD 11-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 5; Length 392;
Best Local Similarity 17.8%; Pred. No. 5.6;
RESULT 1432
ID ADP37455 standard; protein; 394 AA.
DE Human transporter TPM-2.
PN US2003143675-A1.
PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 7; Length 394;
Best Local Similarity 17.8%; Pred. No. 5.6;
RESULT 1433
ID ABO61692 standard; protein; 425 AA.
DE Klebsiella pneumoniae polypeptide seqid 8209.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 81; DB 7; Length 425;
Best Local Similarity 22.7%; Pred. No. 6.3;
RESULT 1434
ID AAR21184 standard; protein; 515 AA.
DE Human TRICH-28 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.8%; Score 81; DB 5; Length 515;
Best Local Similarity 17.8%; Pred. No. 8.1;
RESULT 1435
ID ABU37907 standard; protein; 515 AA.
DE NOVX protein sequence SEQ ID No 60.
PN WO200281517-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 81; DB 6; Length 515;
Best Local Similarity 17.8%; Pred. No. 8.1;
RESULT 1436
ID ADQ66916 standard; protein; 515 AA.
DE Novel human protein sequence #1889.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 81; DB 8; Length 515;
Best Local Similarity 17.8%; Pred. No. 8.1;
RESULT 1437

ID ABO84581 standard; protein; 515 AA.
DE Human cancer-associated protein HP17-001.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.8%; Score 81; DB 8; Length 515;
Best Local Similarity 17.8%; Pred. No. 8.1;
RESULT 1438
ID ADH58563 standard; protein; 516 AA.
DE Human Na+-independent transporter-related transporter protein.
PN WO2003076644-A2.
PD 18-SEP-2003.
PA (APPL-) APPLERA CORP.
Query Match 5.8%; Score 81; DB 7; Length 516;
Best Local Similarity 17.8%; Pred. No. 8.2;
RESULT 1439
ID ADN23220 standard; protein; 544 AA.
DE Bacterial polypeptide #5873.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 81; DB 8; Length 544;
Best Local Similarity 23.0%; Pred. No. 8.8;
RESULT 1440
ID ABB64860 standard; protein; 875 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21372.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 81; DB 4; Length 875;
Best Local Similarity 20.9%; Pred. No. 17;
RESULT 1441
ID ABU39716 standard; protein; 1102 AA.
DE Protein encoded by Prokaryotic essential gene #25243.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 81; DB 6; Length 1102;
Best Local Similarity 20.0%; Pred. No. 23;
RESULT 1442
ID ABO65403 standard; protein; 298 AA.
DE Klebsiella pneumoniae polypeptide seqid 11920.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 80.5; DB 7; Length 298;
Best Local Similarity 18.5%; Pred. No. 4.4;
RESULT 1443
ID ABB32477 standard; protein; 359 AA.
DE Staphylococcus aureus polypeptide SEQ ID NO 14.
PN WO200177365-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 80.5; DB 5; Length 359;
Best Local Similarity 23.4%; Pred. No. 5.7;
RESULT 1444
ID ABM72555 standard; protein; 359 AA.
DE Staphylococcus aureus protein #1795.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.8%; Score 80.5; DB 6; Length 359;
Best Local Similarity 23.4%; Pred. No. 5.7;
RESULT 1445
ID ADC21330 standard; protein; 359 AA.
DE Staphylococcus aureus protein SEQ ID NO: 12.
PN WO2003029484-A2.
PD 10-APR-2003.
PA (PHAA) PHARMACIA & UPJOHN CO.

Query Match 5.8%; Score 80.5; DB 7; Length 359;
 Best Local Similarity 23.4%; Pred. No. 5.7;
 RESULT 1446
 ID ADC25016 standard; protein; 359 AA.
 DE S. aureus polypeptide #6.
 PN US2003087321-A1.
 PD 08-MAY-2003.
 PA (TOMI/) TOMICH C C.
 PA (QUIN/) QUINN C L.
 PA (ARVI/) ARVIDSON S.
 PA (MOTT/) MOTT J E.
 PA (HARR/) HARRIS D W.
 Query Match 5.8%; Score 80.5; DB 7; Length 359;
 Best Local Similarity 23.4%; Pred. No. 5.7;
 RESULT 1447
 ID ADD2518 standard; protein; 359 AA.
 DE Staphylococcus aureus unknown protein #6.
 PN US2003180821-A1.
 PD 25-SEP-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 7; Length 359;
 Best Local Similarity 23.4%; Pred. No. 5.7;
 RESULT 1448
 ID ABB32489 standard; protein; 370 AA.
 DE Staphylococcus aureus polypeptide SEQ ID NO 74.
 PN WO200177365-A2.
 PD 18-OCT-2001.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 5; Length 370;
 Best Local Similarity 23.4%; Pred. No. 5.9;
 RESULT 1449
 ID ADC21396 standard; protein; 370 AA.
 DE Staphylococcus aureus protein SEQ ID NO: 78.
 PN WO2003029484-A2.
 PD 10-APR-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 7; Length 370;
 Best Local Similarity 23.4%; Pred. No. 5.9;
 RESULT 1450
 ID ADC25082 standard; protein; 370 AA.
 DE S. aureus polypeptide #6 encoded by the essential coding region.
 PN US2003087321-A1.
 PD 08-MAY-2003.
 PA (TOMI/) TOMICH C C.
 PA (QUIN/) QUINN C L.
 PA (ARVI/) ARVIDSON S.
 PA (MOTT/) MOTT J E.
 PA (HARR/) HARRIS D W.
 Query Match 5.8%; Score 80.5; DB 7; Length 370;
 Best Local Similarity 23.4%; Pred. No. 5.9;
 RESULT 1451
 ID ADD2584 standard; protein; 370 AA.
 DE Staphylococcus aureus essential protein #22.
 PN US2003180821-A1.
 PD 25-SEP-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 7; Length 370;
 Best Local Similarity 23.4%; Pred. No. 5.9;
 RESULT 1452
 ID ABP38454 standard; protein; 411 AA.
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3299.
 PN US6380370-B1.
 PD 30-APR-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.8%; Score 80.5; DB 5; Length 411;
 Best Local Similarity 22.0%; Pred. No. 6.8;
 RESULT 1453
 ID ADS07146 standard; protein; 411 AA.
 DE Staphylococcus epidermis polypeptide seqid 6441.
 PN US2004147734-A1.
 PD 29-JUL-2004.
 PA (DOUC/) DOUCETTE-STAMM L.
 PA (BUSH/) BUSH D.

Query Match 5.8%; Score 80.5; DB 8; Length 411;
 Best Local Similarity 22.0%; Pred. No. 6.8;
 RESULT 1454
 ID ABU41976 standard; protein; 438 AA.
 DE Protein encoded by Prokaryotic essential gene #27503.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.8%; Score 80.5; DB 6; Length 438;
 Best Local Similarity 18.7%; Pred. No. 7.4;
 RESULT 1455
 ID ADC77508 standard; protein; 458 AA.
 DE Zebrafish TDE1 protein SEQ ID NO:3.
 PN WO2003066829-A2.
 PD 14-AUG-2003.
 PA (DISC-) DISCOVERY GENOMICS INC.
 Query Match 5.8%; Score 80.5; DB 7; Length 458;
 Best Local Similarity 23.3%; Pred. No. 7.9;
 RESULT 1456
 ID ABU39985 standard; protein; 470 AA.
 DE Protein encoded by Prokaryotic essential gene #24512.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.8%; Score 80.5; DB 6; Length 470;
 Best Local Similarity 21.6%; Pred. No. 8.2;
 RESULT 1457
 ID ADS44667 standard; protein; 473 AA.
 DE Bacterial polypeptide #23097.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOV/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.8%; Score 80.5; DB 8; Length 473;
 Best Local Similarity 21.5%; Pred. No. 8.3;
 RESULT 1458
 ID AAU72955 standard; protein; 528 AA.
 DE Neisseria meningitidis virulence protein #45.
 PN WO200185772-A2.
 PD 15-NOV-2001.
 PA (MICR-) MICROSCIENCE LTD.
 Query Match 5.8%; Score 80.5; DB 5; Length 528;
 Best Local Similarity 23.3%; Pred. No. 9.6;
 RESULT 1459
 ID ABP79912 standard; protein; 528 AA.
 DE N. gonorrhoeae amino acid sequence SEQ ID 6354.
 PN WO200279243-A2.
 PD 10-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 5.8%; Score 80.5; DB 6; Length 528;
 Best Local Similarity 23.3%; Pred. No. 9.6;
 RESULT 1460
 ID ABR54218 standard; protein; 531 AA.
 DE Human NOV21a protein SEQ ID NO:104.
 PN WO2003023001-A2.
 PD 20-MAR-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.8%; Score 80.5; DB 6; Length 531;
 Best Local Similarity 19.8%; Pred. No. 9.7;
 RESULT 1461
 ID ADN19054 standard; protein; 590 AA.
 DE Bacterial polypeptide #1707.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOV/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.8%; Score 80.5; DB 8; Length 590;

Best Local Similarity 23.9%; Pred. No. 11;
RESULT 1462
ID ADM25397 standard; protein; 602 AA.
DE Bacterial polypeptide #8050.
PD US2003233675-A1.
PN 18-DEC-2003.
PA (CAOY//) CAO Y.
PA (HINK//) HINKLE G J.
PA (SLAT//) SLATER S C.
PA (CHEN//) CHEN X.
PA (GOLD//) GOLDMAN B S.
Query Match 5.8%; Score 80.5; DB 8; Length 602;
Best Local Similarity 21.5%; Pred. No. 12;
RESULT 1463
ID ADG79602 standard; protein; 137 AA.
DE Human secreted protein of the invention SEQ ID NO:408.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 80; DB 5; Length 137;
Best Local Similarity 24.5%; Pred. No. 1.7;
RESULT 1464
ID ADA54634 standard; protein; 221 AA.
DE Human protein, SEQ ID 2202.
PD EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 80; DB 6; Length 221;
Best Local Similarity 24.5%; Pred. No. 3.3;
RESULT 1465
ID ABU38616 standard; protein; 266 AA.
DE Protein encoded by Prokaryotic essential gene #24143.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 80; DB 6; Length 266;
Best Local Similarity 23.8%; Pred. No. 4.3;
RESULT 1466
ID ADM46298 standard; protein; 271 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID176.
PD WO2004022736-A1.
PD 18-MAR-2004.
PA (NTSC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.7%; Score 80; DB 8; Length 271;
Best Local Similarity 22.2%; Pred. No. 4.4;
RESULT 1467
ID ADK48015 standard; protein; 292 AA.
DE Streptococcus pneumoniae protein, Seq ID No 4530.
PD US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 80; DB 8; Length 292;
Best Local Similarity 18.0%; Pred. No. 4.8;
RESULT 1468
ID AAY38701 standard; protein; 307 AA.
DE Neisseria gonorrhoeae antigen encoded by partial ORF104.
PD WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 5.7%; Score 80; DB 2; Length 307;
Best Local Similarity 20.3%; Pred. No. 5.2;
RESULT 1469
ID ADR94835 standard; protein; 308 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3470.
PD US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 80; DB 8; Length 308;
Best Local Similarity 18.0%; Pred. No. 5.2;
RESULT 1470
ID ABO69264 standard; protein; 325 AA.
DE Pseudomonas aeruginosa polypeptide #1439.
PD US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 80; DB 7; Length 325;
Best Local Similarity 23.8%; Pred. No. 5.6;
RESULT 1471
ID ADN17651 standard; protein; 398 AA.
DE Bacterial polypeptide #304.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY//) CAO Y.
PA (HINK//) HINKLE G J.
PA (SLAT//) SLATER S C.
PA (CHEN//) CHEN X.
PA (GOLD//) GOLDMAN B S.
Query Match 5.7%; Score 80; DB 8; Length 398;
Best Local Similarity 20.4%; Pred. No. 7.4;
RESULT 1472
ID AAY97750 standard; protein; 557 AA.
DE G. oxydans cytochrome C oxidase (COI) protein sequence.
PD EP1103603-A2.
PD 30-MAY-2001.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.7%; Score 80; DB 4; Length 557;
Best Local Similarity 21.2%; Pred. No. 12;
RESULT 1473
ID ADS28294 standard; protein; 902 AA.
DE Bacterial polypeptide #17327.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY//) CAO Y.
PA (HINK//) HINKLE G J.
PA (SLAT//) SLATER S C.
PA (CHEN//) CHEN X.
PA (GOLD//) GOLDMAN B S.
Query Match 5.7%; Score 80; DB 8; Length 902;
Best Local Similarity 26.6%; Pred. No. 23;
RESULT 1474
ID ADA35872 standard; protein; 241 AA.
DE Acinetobacter baumannii protein #3033.
PD US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 79.5; DB 6; Length 241;
Best Local Similarity 24.1%; Pred. No. 4.2;
RESULT 1475
ID ABU16710 standard; protein; 303 AA.
DE Protein encoded by Prokaryotic essential gene #2237.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79.5; DB 6; Length 303;
Best Local Similarity 20.7%; Pred. No. 5.8;
RESULT 1476
ID AAY37819 standard; protein; 305 AA.
DE Amino acid sequence of a Chlamydia trachomatis protein.
PD WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 5.7%; Score 79.5; DB 2; Length 305;
Best Local Similarity 18.0%; Pred. No. 5.9;
RESULT 1477
ID ABU16944 standard; protein; 306 AA.
DE Protein encoded by Prokaryotic essential gene #2471.
PD WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79.5; DB 6; Length 306;
Best Local Similarity 20.4%; Pred. No. 5.9;
RESULT 1478
ID ADA35805 standard; protein; 308 AA.
DE Acinetobacter baumannii protein #2966.
PD US6562958-B1.

PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 79.5; DB 6; Length 308;
Best Local Similarity 20.7%; Pred. No. 5.9;
RESULT 1479
ID ADA33577 standard; protein; 315 AA.
DE Acinetobacter baumannii protein #738.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 79.5; DB 6; Length 315;
Best Local Similarity 20.4%; Pred. No. 6.1;
RESULT 1480
ID AAG71628 standard; protein; 326 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1309.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.7%; Score 79.5; DB 4; Length 326;
Best Local Similarity 19.2%; Pred. No. 6.4;
RESULT 1481
ID ADD69607 standard; protein; 453 AA.
DE Human REMAP protein - SEQ ID 36.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.7%; Score 79.5; DB 7; Length 453;
Best Local Similarity 21.1%; Pred. No. 10;
RESULT 1482
ID AAU43079 standard; protein; 461 AA.
DE Propionibacterium acnes immunogenic protein #3975.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 79.5; DB 4; Length 461;
Best Local Similarity 19.4%; Pred. No. 10;
RESULT 1483
ID ABM39598 standard; protein; 461 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4274.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 79.5; DB 6; Length 461;
Best Local Similarity 19.4%; Pred. No. 10;
RESULT 1484
ID ABO60912 standard; protein; 483 AA.
DE Klebsiella pneumoniae polypeptide seqid 7429.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 79.5; DB 7; Length 483;
Best Local Similarity 25.6%; Pred. No. 11;
RESULT 1485
ID ABU24876 standard; protein; 509 AA.
DE Protein encoded by Prokaryotic essential gene #10403.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79.5; DB 6; Length 509;
Best Local Similarity 23.0%; Pred. No. 12;
RESULT 1486
ID AAB96516 standard; protein; 513 AA.
DE Putative P. abyssi hydrogenase subunit #5.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 5.7%; Score 79.5; DB 4; Length 513;
Best Local Similarity 19.9%; Pred. No. 12;
RESULT 1487
ID ADO28948 standard; protein; 630 AA.
DE Mouse novel GPCR PGR25, SEQ ID NO:47.

PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.7%; Score 79.5; DB 8; Length 630;
Best Local Similarity 20.8%; Pred. No. 16;
RESULT 1488
ID ABB67845 standard; protein; 2210 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30327.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 5.7%; Score 79.5; DB 4; Length 2210;
Best Local Similarity 24.5%; Pred. No. 90;
RESULT 1489
ID ABU40578 standard; protein; 292 AA.
DE Protein encoded by Prokaryotic essential gene #26105.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79; DB 6; Length 292;
Best Local Similarity 16.5%; Pred. No. 6.3;
RESULT 1490
ID AAY90241 standard; protein; 293 AA.
DE Chlamydia antigen CPN100708.
PN WO200032794-A2.
PD 08-JUN-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 5.7%; Score 79; DB 3; Length 293;
Best Local Similarity 18.3%; Pred. No. 6.3;
RESULT 1491
ID ABP62011 standard; protein; 293 AA.
DE C. pneumoniae BVH-CPN19 from strain CWL-029.
PN EP1219635-A2.
PD 03-JUL-2002.
PA (SHIR-) SHIRE BIOCHEM INC.
Query Match 5.7%; Score 79; DB 5; Length 293;
Best Local Similarity 18.3%; Pred. No. 6.3;
RESULT 1492
ID AAY38700 standard; protein; 307 AA.
DE Neisseria meningitidis strain A antigen encoded by ORF104.
PN WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 5.7%; Score 79; DB 2; Length 307;
Best Local Similarity 21.5%; Pred. No. 6.7;
RESULT 1493
ID ADH42479 standard; protein; 308 AA.
DE Novel human protein NOV69a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 79; DB 8; Length 308;
Best Local Similarity 19.3%; Pred. No. 6.8;
RESULT 1494
ID AAG44352 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55545.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 79; DB 3; Length 363;
Best Local Similarity 25.9%; Pred. No. 8.5;
RESULT 1495
ID AAG44351 standard; protein; 373 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55544.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 79; DB 3; Length 373;
Best Local Similarity 25.9%; Pred. No. 8.8;
RESULT 1496
ID AAG44350 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55543.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 79; DB 3; Length 377;

Best Local Similarity 25.9%; Pred. No. 9;
RESULT 1497
ID ABU20479 standard; protein; 389 AA.
DE Protein encoded by Prokaryotic essential gene #6006.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79; DB 6; Length 389;
Best Local Similarity 20.1%; Pred. No. 9.3;
RESULT 1498
ID ADN20367 standard; protein; 390 AA.
DE Bacterial polypeptide #3020.
FN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 79; DB 8; Length 390;
Best Local Similarity 21.5%; Pred. No. 9.4;
RESULT 1499
ID ADO29107 standard; protein; 416 AA.
DE Mouse novel GPCR HCTR1, SEQ ID NO:206.
FN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.7%; Score 79; DB 8; Length 416;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 1500
ID ABU23067 standard; protein; 444 AA.
DE Protein encoded by Prokaryotic essential gene #8594.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79; DB 6; Length 444;
Best Local Similarity 21.6%; Pred. No. 11;

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OM protein - protein search, using sw model

Run on: August 26, 2005, 17:12:21 ; Search time 41 Seconds
(without alignment)
624.236 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MWFQQLSFLPSALVIWTS.....YDTAPCPINNERTLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361.5	26.0	246	2	T13747
2	288	20.7	271	2	T19654
3	120	8.6	547	2	C88456
4	103	7.4	332	2	E69312
5	98.5	7.1	1120	2	A10561
6	97	7.0	604	2	E72523
7	96	6.9	495	2	S43882
8	94	6.8	495	1	S16447
9	93.5	6.7	379	2	D96506
10	93.5	6.7	429	2	F71651
11	93	6.7	1120	2	F90693
12	93	6.7	1120	2	B85544
13	93	6.7	1120	2	H64776
14	92.5	6.6	473	2	A50801
15	91.5	6.6	373	2	T24487
16	91.5	6.6	712	2	T02479
17	90.5	6.5	614	2	E86194
18	90	6.5	400	2	C82503
19	90	6.5	492	2	S89107
20	90	6.5	528	2	S19366
21	89.5	6.4	440	2	B64090
22	89.5	6.4	443	2	A81706
23	89.5	6.4	495	2	G71019
24	89.5	6.4	599	2	T24333
25	89	6.4	428	2	A10034
26	89	6.4	757	2	T42693
27	88.5	6.4	430	2	E75217
28	88.5	6.4	844	2	T23656
29	88	6.3	1165	2	A46180

30	87.5	6.3	233	2	E70114
31	87.5	6.3	429	2	D82181
32	87.5	6.3	482	2	B69803
33	87.5	6.3	540	2	T24875
34	87	6.2	396	2	B91013
35	87	6.2	396	2	D85857
36	87	6.2	435	2	C95975
37	87	6.2	613	2	C83496
38	86.5	6.2	400	2	C69757
39	86.5	6.2	583	2	AH1151
40	86.5	6.2	770	2	G72589
41	86	6.2	373	2	D89865
42	86	6.2	389	2	G75133
43	86	6.2	396	1	E64987
44	86	6.2	703	2	B86146
45	85.5	6.1	295	2	B81179
46	85.5	6.1	296	2	AB0210
47	85.5	6.1	498	2	S78184
48	85	6.1	338	2	G70584
49	85	6.1	443	2	B86849
50	85	6.1	1180	2	A47202
51	84.5	6.1	457	2	T46332
52	84.5	6.1	463	2	AH0189
53	84.5	6.1	479	2	D72354
54	84.5	6.1	491	2	T15605
55	84.5	6.1	638	2	T11801
56	84.5	6.1	765	2	T22800
57	84	6.0	318	2	E95218
58	84	6.0	460	2	A71028
59	84	6.0	575	2	B83586
60	84	6.0	597	2	H82328
61	83.5	6.0	261	2	D64166
62	83.5	6.0	295	2	A81927
63	83.5	6.0	521	2	T41621
64	83.5	6.0	638	2	B34285
65	83	6.0	305	2	AD1998
66	83	6.0	318	2	C98082
67	83	6.0	427	2	F97790
68	83	6.0	460	2	D75106
69	83	6.0	496	2	B83503
70	83	6.0	637	2	S01509
71	82.5	5.9	391	2	S48967
72	82.5	5.9	418	2	B83175
73	82.5	5.9	452	2	A71877
74	82.5	5.9	494	2	T14246
75	82.5	5.9	596	2	S46001
76	82	5.9	317	2	D84098
77	82	5.9	327	2	A82241
78	82	5.9	356	2	D86408
79	82	5.9	446	2	A38244
80	82	5.9	461	2	H64636
81	82	5.9	548	2	B87423
82	82	5.9	557	2	T41588
83	82	5.9	573	2	T23589
84	82	5.9	693	2	T19598
85	82	5.9	1139	2	A10379
86	81.5	5.9	205	2	D95200
87	81.5	5.9	205	2	C98067
88	81.5	5.9	292	2	AE1539
89	81.5	5.9	307	2	H97018
90	81.5	5.9	351	2	C86408
91	81.5	5.9	438	2	B83017
92	81.5	5.9	485	2	T24677
93	81.5	5.9	486	2	S51503
94	81.5	5.9	734	2	T13785
95	81	5.8	293	2	C95892
96	81	5.8	293	2	D71517
97	81	5.8	438	2	H85822
98	81	5.8	479	2	C64878
99	81	5.8	479	2	T44326
100	81	5.8	487	2	E96782
101	81	5.8	544	2	T24633
102	81	5.8	710	2	T12143

hemolysin III (ypl
GDEF family prote
metabolite transpo
hypothetical prote
bicyclomycin resis
bicyclomycin resis
probable polysacch
glutathione-regula
transporter homolo
glycerophosphoryl
hypothetical prote
hypothetical prote
hypothetical prote
bicyclomycin resis
F22L4.12 protein -
spermidine/putresc
probable ABC sugar
NADH2 dehydrogenas
phosphate transpor
polysaccharide bios
adenylate cyclase
hypothetical prote
Amino acid permeas
lipopolysaccharide
hypothetical prote
NADH2 dehydrogenas
hypothetical prote
iron-compound ABC
hypothetical prote
probable permease
hypothetical prote
hypothetical prote
probable polyamine
hypothetical prote
NADH2 dehydrogenas
hypothetical prote
hypothetical prote
putrescine-ornithi
hypothetical prote
probable amino aci
NADH2 dehydrogenas
ethanolaminephosph
probable aromatic
proline/betaine tr
NADH2 dehydrogenas
probable amino aci
hypothetical prote
probable ABC trans
purine permease [i
citrate transport
proline/betaine tr
cytochrome-c oxida
probable amino-aci
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypochet
hypothetical prote
sugar ABC transpor
bacitracin resista
F3H9.12 protein -
probable MFS trans
hypothetical prote
NADH2 dehydrogenas
NADH2 dehydrogenas
probable glycerol-
probable metal tra
probable transport
probable amino aci
hypothetical prote
hypothetical prote
NADH2 dehydrogenas

103	80.5	5.8	359	2	F90055	conserved hypothet	176	77.5	5.6	363	2	A72771	hypothetical prote
104	80.5	5.8	385	2	T07130	probable amino aci	177	77.5	5.6	461	2	H85755	probable amino aci
105	80.5	5.8	433	2	AC0043	anaerobic C4-dicar	178	77.5	5.6	464	2	C83605	probable transport
106	80.5	5.8	473	2	G69789	sugar transporter	179	77.5	5.6	479	2	A90863	probable amino aci
107	80.5	5.8	528	2	E81186	L-lactate permease	180	77.5	5.6	499	2	A90882	probable amino aci
108	80.5	5.8	590	1	QRBYPR	arginine transport	181	77.5	5.6	506	2	F64862	hypothetical prote
109	80.5	5.8	637	2	S78171	heme lyase YefJr -	182	77.5	5.6	510	2	D96741	hypothetical prote
110	80.5	5.8	728	2	T13794	NADH2 dehydrogenas	183	77.5	5.6	510	2	E71695	hypothetical prote
111	80	5.7	266	2	G83178	conserved hypothet	184	77.5	5.6	513	2	A82432	sodium/solute symp
112	80	5.7	291	2	A97387	hypothetical prote	185	77.5	5.6	526	2	T01853	probable hexose tr
113	80	5.7	291	2	AB2605	hypothetical prote	186	77.5	5.6	532	1	S49345	cytochrome-c oxida
114	80	5.7	429	1	C41903	arsenical pump mem	187	77.5	5.6	535	2	S76103	hypothetical prote
115	80	5.7	702	2	T12141	NADH2 dehydrogenas	188	77.5	5.6	649	2	A69478	NADH2 dehydrogenas
116	80	5.7	902	2	C83964	cation-transportin	189	77.5	5.6	717	2	T46172	phenylalanine ammo
117	80	5.7	1123	2	T48586	hypothetical prote	190	77.5	5.6	1118	2	B83018	conserved hypothet
118	79.5	5.7	323	2	T32279	hypothetical prote	191	77	5.5	282	2	AD1231	B. subtilis YxkD p
119	79.5	5.7	405	2	T42992	cyclin D - Caenorh	192	77	5.5	332	2	D95973	probable sugar upt
120	79.5	5.7	445	2	S77010	nickel resistance	193	77	5.5	417	2	F90270	amino acid permeas
121	79.5	5.7	499	2	F75059	NADH-dehydrogenase	194	77	5.5	438	2	B69855	shikimate transport
122	79.5	5.7	539	1	S49495	cytochrome-c oxida	195	77	5.5	438	2	G64962	phosphate transpor
123	79.5	5.7	542	2	AG3605	potassium efflux s	196	77	5.5	471	2	H90502	membrane protein S
124	79.5	5.7	570	2	AH2765	cytochrome c oxida	197	77	5.5	519	2	JQ0124	cytochrome-c oxida
125	79.5	5.7	598	2	E97546	NADH2 dehydrogenas	198	77	5.5	551	1	A55582	hypothetical prote
126	79.5	5.7	741	2	T13051	Na+/H+-exchanging	199	77	5.5	579	2	AB2177	bo-type ubiquinol
127	79.5	5.7	831	2	B40204	NADH2 dehydrogenas	200	77	5.5	662	2	H84984	hypothetical prote
128	79	5.7	172	2	S55015	NADH2 dehydrogenas	201	77	5.5	710	2	T20635	hypothetical prote
129	79	5.7	183	2	A64009	hypothetical prote	202	77	5.5	739	2	T13038	NADH2 dehydrogenas
130	79	5.7	281	2	T26244	hypothetical prote	203	77	5.5	749	2	E71275	hypothetical integ
131	79	5.7	293	2	B83783	hypothetical prote	204	77	5.5	915	2	H96709	hypothetical prote
132	79	5.7	293	2	H72064	ABC transporter, p	205	77	5.5	936	2	T26521	hypothetical prote
133	79	5.7	293	2	C86558	metal transport, pr	206	76.5	5.5	152	2	C72681	hypothetical prote
134	79	5.7	307	2	C81862	conserved hypothet	207	76.5	5.5	269	2	H69768	conserved hypothet
135	79	5.7	377	2	T49063	nodulin-like prote	208	76.5	5.5	284	2	G64052	probable formate t
136	79	5.7	390	2	H72285	hypothetical prote	209	76.5	5.5	289	2	T02095	transmembrane prot
137	79	5.7	395	2	D69312	molybdopterin oxid	210	76.5	5.5	300	2	S40858	hypothetical 32.9K
138	79	5.7	410	2	E84998	hypothetical prote	211	76.5	5.5	300	2	H91233	probable transport
139	79	5.7	438	2	B90976	shikimate transport	212	76.5	5.5	302	2	H86080	probable transport
140	79	5.7	444	2	G82392	conserved hypothet	213	76.5	5.5	301	2	B82235	conserved hypothet
141	79	5.7	453	2	AF1198	conserved hypothet	214	76.5	5.5	301	2	T27585	hypothetical prote
142	79	5.7	473	2	T31717	hypothetical prote	215	76.5	5.5	305	2	D83699	hypothetical prote
143	79	5.7	489	2	T97289	lysine-specific pe	216	76.5	5.5	334	2	A75142	oligopeptide trans
144	79	5.7	685	2	T12139	NADH2 dehydrogenas	217	76.5	5.5	370	2	AB3334	daunorubicin resis
145	79	5.7	819	2	G69801	hypothetical prote	218	76.5	5.5	377	2	C89456	Na+/H+ antiporter
146	79	5.7	2198	2	T20371	hypothetical prote	219	76.5	5.5	382	2	B82177	probable membrane
147	78.5	5.6	169	2	H84191	hypothetical prote	220	76.5	5.5	395	2	AD0678	probable membrane
148	78.5	5.6	241	2	S00836	mcbE protein - Esc	221	76.5	5.5	431	2	H84069	hypothetical prote
149	78.5	5.6	366	2	C64449	cationic amino aci	222	76.5	5.5	474	2	F64119	NAD(P) transhydrog
150	78.5	5.6	405	2	T26678	hypothetical prote	223	76.5	5.5	475	2	E69643	histidine permease
151	78.5	5.6	412	2	G89773	hypothetical prote	224	76.5	5.5	495	2	AD0402	glycerol kinase (E
152	78.5	5.6	493	2	F75113	NADH dehydrogenase	225	76.5	5.5	548	2	B72542	probable cytochrom
153	78.5	5.6	579	2	A70954	hypothetical prote	226	76.5	5.5	725	2	S64124	probable membrane
154	78.5	5.6	622	2	E69609	cytochrome-c oxida	227	76.5	5.5	746	2	T13698	NADH2 dehydrogenas
155	78.5	5.6	624	2	T48587	peptide transporte	228	76.5	5.5	855	2	T47534	hypothetical prote
156	78.5	5.6	732	2	T13814	NADH2 dehydrogenas	229	76.5	5.5	1187	2	T20544	hypothetical prote
157	78.5	5.6	744	2	T13485	NADH2 dehydrogenas	230	76.5	5.5	1342	2	E85614	cell division prot
158	78.5	5.6	1325	2	T01037	hypothetical prote	231	76.5	5.5	1342	2	G90750	cell division prot
159	78	5.6	158	2	T26539	hypothetical prote	232	76	5.5	261	2	A64066	probable membrane
160	78	5.6	307	2	D81082	conserved hypothet	233	76	5.5	275	2	C97028	probable metal-bin
161	78	5.6	335	2	E81736	phospho-N-acetylmu	234	76	5.5	281	2	AB1585	B. subtilis YxkD p
162	78	5.6	382	2	E37742	hypothetical prote	235	76	5.5	282	2	D97767	hypothetical prote
163	78	5.6	388	2	G75375	hypothetical prote	236	76	5.5	336	2	T23902	hypothetical prote
164	78	5.6	396	2	AF0785	bicyclomycin resis	237	76	5.5	365	2	F82210	amino acid ABC tra
165	78	5.6	414	2	S53075	probable membrane	238	76	5.5	415	2	G83568	probable permease
166	78	5.6	422	2	H64489	hypothetical prote	239	76	5.5	447	2	C84306	hypothetical prote
167	78	5.6	462	2	T48661	acetate-CoA ligase	240	76	5.5	452	2	S46037	prephenate dehydro
168	78	5.6	688	2	T06299	potassium transpor	241	76	5.5	480	2	G83414	cytochrome-c oxida
169	78	5.6	701	2	T15238	hypothetical prote	242	76	5.5	502	2	JN0113	nicotinic acetylch
170	77.5	5.6	212	2	B83936	hypothetical prote	243	76	5.5	558	2	S08270	cytochrome-c oxida
171	77.5	5.6	283	2	H95887	probable ABC trans	244	76	5.5	578	2	T13664	NADH2 dehydrogenas
172	77.5	5.6	292	2	AD1182	sugar ABC transpor	245	76	5.5	617	2	T20409	hypothetical prote
173	77.5	5.6	293	2	AH0143	probable membrane	246	76	5.5	659	2	E85889	hypothetical prote
174	77.5	5.6	296	2	C95326	AttA2-like ABC tra	247	76	5.5	659	2	B91045	probable oxidoredu
175	77.5	5.6	335	2	A72289	oligopeptide ABC t	248	76	5.5	669	1	DNMUU5	NADH2 dehydrogenas

249	76	5.5	956	2	A89153	protein C24B5.3 [i	322	74.5	5.4	411	2	T03836	phosphate/phospho
250	76	5.5	958	2	AC0204	probable integral	323	74.5	5.4	439	2	AB0389	branched-chain ami
251	76	5.5	966	2	H97717	hypothetical prote	324	74.5	5.4	447	2	T19112	hypothetical prote
252	76	5.5	971	2	H71719	hypothetical prote	325	74.5	5.4	469	1	BDEC	melibiose carrier
253	76	5.5	1052	2	T50127	hypothetical prote	326	74.5	5.4	469	2	C86107	melibiose permease
254	76	5.5	1074	2	T45094	probable arabinosy	327	74.5	5.4	469	2	F91266	probable amino-aci
255	76	5.5	1166	2	T49201	adenylate cyclase	328	74.5	5.4	476	2	AG0502	hypothetical prote
256	75.5	5.4	210	2	T01623	hypothetical prote	329	74.5	5.4	544	2	T32895	hypothetical prote
257	75.5	5.4	237	2	A99737	hypothetical prote	330	74.5	5.4	560	2	T32727	NADH2 dehydrogenas
258	75.5	5.4	237	2	B85587	hypothetical prote	331	74.5	5.4	726	2	T12215	two-component hybr
259	75.5	5.4	240	2	D71939	hypothetical prote	332	74.5	5.4	889	2	AD2215	probable membrane
260	75.5	5.4	252	2	B47188	MHC class II histo	333	74.5	5.4	953	2	S19427	conserved hypoteth
261	75.5	5.4	295	1	Q0SABT	hypothetical prote	334	74	5.3	277	2	E72030	CT560 hypothetical
262	75.5	5.4	296	2	E83049	conserved hypoteth	335	74	5.3	281	2	A86594	transcriptional repr
263	75.5	5.4	297	2	AE0400	probable membrane	336	74	5.3	281	2	H90387	hypothetical prote
264	75.5	5.4	322	2	A97657	ferrichrome ABC tr	337	74	5.3	286	2	C69635	transcriptional repr
265	75.5	5.4	322	2	A12880	ABC transporter, m	338	74	5.3	303	2	T25501	hypothetical prote
266	75.5	5.4	338	2	C83785	ferrichrome ABC tr	339	74	5.3	322	1	A29928	membrane-associate
267	75.5	5.4	397	2	D69538	arsenite transport	340	74	5.3	370	2	H84351	hypothetical prote
268	75.5	5.4	432	2	A42476	hypothetical prote	341	74	5.3	380	2	S34964	rbc protein - Shig
269	75.5	5.4	432	2	AD0766	probable O-antigen	342	74	5.3	400	2	F86887	hypothetical prote
270	75.5	5.4	441	2	B71027	probable nfpD prot	343	74	5.3	401	2	E82951	probable MFS trans
271	75.5	5.4	454	2	E85826	probable amino aci	344	74	5.3	404	2	A36865	ammonium transport
272	75.5	5.4	454	2	H90980	probable amino aci	345	74	5.3	407	2	G81010	conserved hypoteth
273	75.5	5.4	454	2	E64966	probable amino aci	346	74	5.3	425	2	H11554	hypothetical prote
274	75.5	5.4	454	2	AG0763	probable amino aci	347	74	5.3	431	2	T41614	malate permease -
275	75.5	5.4	459	2	S42238	tetracycline resist	348	74	5.3	437	2	G82032	probable permease
276	75.5	5.4	476	2	S23576	melibiose transpor	349	74	5.3	446	2	A42661	citrate carrier pr
277	75.5	5.4	492	2	AC0768	probable transmemb	350	74	5.3	446	2	AD0509	citrate-sodium sym
278	75.5	5.4	513	2	T39554	hypothetical prote	351	74	5.3	446	2	B42661	citrate carrier pr
279	75.5	5.4	532	2	D95287	conserved hypoteth	352	74	5.3	459	2	T11084	NADH2 dehydrogenas
280	75.5	5.4	567	2	B81408	probable thiol-dis	353	74	5.3	473	2	AG0948	probable membrane
281	75.5	5.4	676	1	S54750	cytochrome c-type	354	74	5.3	508	2	A83839	hypothetical prote
282	75.5	5.4	735	2	F84726	probable Na+/H+ an	355	74	5.3	530	2	F85768	PTS system, maltos
283	75.5	5.4	740	2	T12223	NADH2 dehydrogenas	356	74	5.3	530	2	A99920	PTS system, maltos
284	75.5	5.4	832	2	A40205	Na+/H+-exchanging	357	74	5.3	532	2	F90457	hypothetical prote
285	75.5	5.4	914	2	T40529	penicillin-binding	358	74	5.3	542	2	H96840	hypothetical prote
286	75.5	5.4	932	2	T25941	hypothetical prote	359	74	5.3	592	2	T25837	hypothetical prote
287	75	5.4	262	2	B83827	hypothetical prote	360	74	5.3	612	2	C90419	glucan 1,4 alpha g
288	75	5.4	289	2	T12037	probable aquaporin	361	74	5.3	740	2	AH0600	probable membrane
289	75	5.4	291	2	T04139	transmembrane prot	362	74	5.3	817	2	TS1787	hypothetical prote
290	75	5.4	298	2	S75972	hypothetical prote	363	74	5.3	908	2	S51293	probable membrane
291	75	5.4	322	2	B98193	sugar ABC transport	364	74	5.3	947	2	H85088	hypothetical prote
292	75	5.4	322	2	AH3093	hypothetical prote	365	73.5	5.3	218	1	D69372	osmoprotection pro
293	75	5.4	395	2	S73531	CNP-diglyceride sy	366	73.5	5.3	240	2	A64652	hypothetical prote
294	75	5.4	398	2	B71193	hypothetical prote	367	73.5	5.3	299	2	B83323	probable branched
295	75	5.4	429	1	B41902	arsenical pump mem	368	73.5	5.3	329	2	AD0442	hypothetical prote
296	75	5.4	432	2	H71092	hypothetical prote	369	73.5	5.3	337	2	T23942	hypothetical prote
297	75	5.4	451	2	E90171	inorganic phosphat	370	73.5	5.3	343	2	G86709	hypothetical prote
298	75	5.4	461	2	AF1179	hexose phosphate t	371	73.5	5.3	363	2	AF2457	hypothetical prote
299	75	5.4	494	2	A82234	probable carbon at	372	73.5	5.3	372	2	A98157	probable permease
300	75	5.4	507	2	A11739	amino acid antipor	373	73.5	5.3	372	2	AH3130	ABC transporter, m
301	75	5.4	559	2	T33168	hypothetical prote	374	73.5	5.3	391	2	S30046	potassium channel
302	75	5.4	599	2	T48383	uracil transporter	375	73.5	5.3	409	2	T03718	suppressor 2 prote
303	75	5.4	625	2	D45335	cytochrome-c oxida	376	73.5	5.3	423	2	C81266	probable efflux pr
304	75	5.4	643	2	E69373	conserved hypoteth	377	73.5	5.3	425	2	C65100	hypothetical 46.6
305	75	5.4	917	2	T49699	glycoprotein 130 -	378	73.5	5.3	426	2	D72049	phosphate permease
306	75	5.4	1056	2	G84865	hypothetical prote	379	73.5	5.3	443	2	F85972	probable transport
307	75	5.4	1294	2	S77690	probable membrane	380	73.5	5.3	443	2	G91127	probable transport
308	74.5	5.4	174	2	F90494	conserved hypoteth	381	73.5	5.3	463	2	F90285	metabolite transpo
309	74.5	5.4	288	2	T09794	major intrinsic pr	382	73.5	5.3	476	2	AC1023	melibiose carrier
310	74.5	5.4	293	2	A96209	motC protein [limp	383	73.5	5.3	477	2	F82200	cytochrome-c oxida
311	74.5	5.4	293	2	AH3077	hypothetical prote	384	73.5	5.3	498	2	F89861	Na+/H+-antipor
312	74.5	5.4	305	2	B33465	lic-1 protein B -	385	73.5	5.3	507	2	B97765	adp ATP carrier pr
313	74.5	5.4	311	2	F70184	ribose/galactose A	386	73.5	5.3	522	2	D86263	F13K23.21 protein
314	74.5	5.4	323	2	T31697	hypothetical prote	387	73.5	5.3	526	2	S74025	conserved hypoteth
315	74.5	5.4	324	1	C47691	phospho-N-acetylmu	388	73.5	5.3	526	2	T29433	hypothetical prote
316	74.5	5.4	325	2	F82558	lipopolysaccharide	389	73.5	5.3	547	2	AB2639	pH adaptation potass
317	74.5	5.4	366	2	H86614	CT838 hypothetical	390	73.5	5.3	548	2	C97421	phad protein (X933
318	74.5	5.4	366	2	C72009	conserved hypoteth	391	73.5	5.3	592	2	E75032	carbon starvation
319	74.5	5.4	367	2	T13813	NADH2 dehydrogenas	392	73.5	5.3	607	2	S19585	seroconin transpor
320	74.5	5.4	399	2	T27853	hypothetical prote	393	73.5	5.3	607	2	S63395	probable membrane
321	74.5	5.4	409	1	F69814	fosmidmycin resist	394	73.5	5.3	630	2	S30604	neurotransmitter t

395	73.5	5.3	674	2	B82954	conserved hypotet	468	72.5	5.2	741	2	T13085	NADH2 dehydrogenas
396	73.5	5.3	699	2	T13730	NADH2 dehydrogenas	469	72.5	5.2	743	2	T13073	NADH2 dehydrogenas
397	73.5	5.3	875	2	H90371	proteinase [import	470	72.5	5.2	744	2	T13040	NADH2 dehydrogenas
398	73.5	5.3	885	2	B69783	transporter homolo	471	72.5	5.2	744	2	T13757	NADH2 dehydrogenas
399	73.5	5.3	889	2	T20123	hypothetical prote	472	72.5	5.2	917	2	T17244	hypothetical prote
400	73.5	5.3	1099	2	A55405	adenylate cyclase	473	72.5	5.2	923	2	C97487	hypothetical prote
401	73.5	5.3	1128	2	T04922	hypothetical prote	474	72.5	5.2	923	2	AC2705	conserved hypotet
402	73.5	5.3	1343	2	AF0611	cell division prot	475	72.5	5.2	953	2	S54478	probable membrane
403	73.5	5.3	1343	2	B55282	neurofibromatosis-	476	72.5	5.2	958	2	A70634	probable mmp11 pro
404	73.5	5.3	2820	2	JC5196	neurofibromin I -	477	72.5	5.2	978	2	JC8067	mitochondrial Cl-t
405	73.5	5.3	2825	2	I54352	neurofibromin I -	478	72.5	5.2	1148	2	H90175	NADH dehydrogenase
406	73	5.2	140	2	C81199	hypothetical prote	479	72.5	5.2	1329	2	A64828	cell division prot
407	73	5.2	193	2	B91170	hypothetical membr	480	72.5	5.2	2658	2	A86216	protein T23G18.2 [
408	73	5.2	193	2	B86016	hypothetical prote	481	72	5.2	215	2	F75166	hypothetical prote
409	73	5.2	261	2	AC0251	high-affinity zinc	482	72	5.2	242	2	S49598	membrane protein -
410	73	5.2	262	2	F97151	ABC transported MD	483	72	5.2	249	2	A71234	hypothetical prote
411	73	5.2	282	2	H71696	hypothetical prote	484	72	5.2	252	2	A71165	hypothetical prote
412	73	5.2	283	2	D83009	probable permease	485	72	5.2	257	2	AC1024	probable dimethyl
413	73	5.2	292	2	C95147	licB protein [impo	486	72	5.2	260	1	WMVZP0	FP0 protein - fowl
414	73	5.2	294	2	D81434	probable 4-hydroxy	487	72	5.2	261	2	S62047	probable membrane
415	73	5.2	286	2	A98015	hypothetical prote	488	72	5.2	282	2	D98058	hypothetical prote
416	73	5.2	301	2	AH2064	hypothetical prote	489	72	5.2	286	2	T23066	hypothetical prote
417	73	5.2	311	2	T33436	hypothetical prote	490	72	5.2	315	2	B83778	hypothetical prote
418	73	5.2	364	2	D95959	conserved hypotet	491	72	5.2	339	2	E86761	ferrichrome ABC tr
419	73	5.2	384	2	S37608	NADH2 dehydrogenas	492	72	5.2	339	2	T23244	conserved hypotet
420	73	5.2	399	2	AE0396	probable sugar tra	493	72	5.2	355	2	A55733	G protein-coupled
421	73	5.2	401	2	T49329	hypothetical prote	494	72	5.2	359	2	AF3044	hypothetical prote
422	73	5.2	436	2	S77639	exopolysaccharide	495	72	5.2	361	2	C84246	hypothetical prote
423	73	5.2	437	2	D86633	amino acid permeas	496	72	5.2	367	2	C82943	ribose ABC transpo
424	73	5.2	453	2	AD1556	conserved hypotet	497	72	5.2	374	2	F98241	ferrichrome ABC tr
425	73	5.2	456	2	H97735	hypothetical prote	498	72	5.2	378	2	T34372	mtk protein (AF00
426	73	5.2	470	2	B86118	transport of D-ala	499	72	5.2	417	2	F90916	hypothetical prote
427	73	5.2	470	2	B91277	D-serine/D-alanine	500	72	5.2	417	2	F64915	membrane protein Y
428	73	5.2	470	2	S56433	D-serine/D-alanine	501	72	5.2	417	2	C85765	probable transport
429	73	5.2	495	1	S25942	NADH2 dehydrogenas	502	72	5.2	421	2	B84129	ammonium transport
430	73	5.2	507	2	AB1370	amino acid antiport	503	72	5.2	431	2	C82432	sugar transporter
431	73	5.2	574	2	T05964	probable low-affin	504	72	5.2	440	2	C75107	modulation protein
432	73	5.2	633	2	T19189	hypothetical prote	505	72	5.2	440	2	C82410	conserved hypotet
433	73	5.2	639	2	G88839	protein ClOC6.5 [i	506	72	5.2	444	2	T24076	hypothetical prote
434	73	5.2	700	2	T13668	NADH2 dehydrogenas	507	72	5.2	447	2	AE0094	probable gluconate
435	73	5.2	732	2	T14233	NADH2 dehydrogenas	508	72	5.2	453	2	H71732	cytochrome D ubiqu
436	73	5.2	1564	2	T27121	hypothetical prote	509	72	5.2	463	2	H69822	sodium-glutamate s
437	73	5.2	3079	1	RGBY12	probable GTPase-ac	510	72	5.2	482	2	T17022	NADH2 dehydrogenas
438	73	5.2	3898	1	GNWVHB	genome polypeptide	511	72	5.2	507	2	B71695	adp, ATP carrier p
439	72.5	5.2	118	2	G64394	hypothetical prote	512	72	5.2	524	2	AD1897	hypothetical prote
440	72.5	5.2	235	2	F95230	membrane protein [513	72	5.2	530	1	G64918	phosphotransferase
441	72.5	5.2	235	2	A99095	conserved hypotet	514	72	5.2	530	2	T51836	high affinity nitr
442	72.5	5.2	235	2	AF0598	probable membrane	515	72	5.2	582	2	H96604	probable 3'-5' exo
443	72.5	5.2	271	2	T11704	NADH2 dehydrogenas	516	72	5.2	602	2	AC2313	hypothetical prote
444	72.5	5.2	284	2	AH0680	probable dimethyl	517	72	5.2	608	2	S76192	hypothetical prote
445	72.5	5.2	286	2	B99213	cytochrome C oxida	518	72	5.2	614	2	T13727	NADH2 dehydrogenas
446	72.5	5.2	297	2	F82039	ribonuclease BN VC	519	72	5.2	620	2	F83976	cytochrome-c oxida
447	72.5	5.2	308	2	AF0461	probable membrane	520	72	5.2	628	2	AG2707	hypothetical prote
448	72.5	5.2	330	2	D95902	probable sugar ABC	521	72	5.2	629	2	H97489	mitochondrial tran
449	72.5	5.2	347	2	AD2201	hypothetical prote	522	72	5.2	641	2	AG2164	hypothetical prote
450	72.5	5.2	368	2	T13815	NADH2 dehydrogenas	523	72	5.2	644	2	B97885	transporter, trunc
451	72.5	5.2	375	2	B40205	Na+/H+-exchangin	524	72	5.2	681	2	T13566	NADH2 dehydrogenas
452	72.5	5.2	421	2	T22969	hypothetical prote	525	72	5.2	689	2	T11917	NADH2 dehydrogenas
453	72.5	5.2	434	2	D65132	hypothetical 4.6.5	526	72	5.2	692	2	T33786	hypothetical prote
454	72.5	5.2	454	2	B90623	NADH dehydrogenase	527	72	5.2	696	2	T12160	hypothetical prote
455	72.5	5.2	458	2	T19110	hypothetical prote	528	72	5.2	698	2	T12565	NADH2 dehydrogenas
456	72.5	5.2	461	2	G85059	probable sugar tra	529	72	5.2	698	2	T12161	NADH2 dehydrogenas
457	72.5	5.2	461	2	S75711	hypothetical prote	530	72	5.2	700	2	T13763	NADH2 dehydrogenas
458	72.5	5.2	491	2	H83979	lysine decarboxyla	531	72	5.2	719	2	T13793	NADH2 dehydrogenas
459	72.5	5.2	494	1	F69355	Na+/H+ antiporter	532	72	5.2	796	2	S62464	coatomer complex b
460	72.5	5.2	498	2	B89832	hypothetical prote	533	72	5.2	906	2	S35312	RNA1 polypeptide -
461	72.5	5.2	523	2	A11970	hypothetical prote	534	72	5.2	2150	2	T08165	hypothetical prote
462	72.5	5.2	615	2	S77084	ABC-type transport	535	71.5	5.1	213	2	A71049	hypothetical prote
463	72.5	5.2	645	2	B70001	ABC transporter (p	536	71.5	5.1	232	2	E86825	phosphatidate cyti
464	72.5	5.2	682	2	T12715	NADH2 dehydrogenas	537	71.5	5.1	260	2	H89899	hypothetical prote
465	72.5	5.2	684	2	T13491	NADH2 dehydrogenas	538	71.5	5.1	281	2	A55862	aarA protein - Pro
466	72.5	5.2	704	2	T13665	NADH2 dehydrogenas	539	71.5	5.1	283	2	B97769	hypothetical prote
467	72.5	5.2	736	2	T12716	NADH2 dehydrogenas	540	71.5	5.1	285	2	A11127	Staphylococcus xyl

541	71.5	5.1	295	2	AB0462	sn-glycerol-3-phos	614	71	5.1	468	2	D83625	probable transport
542	71.5	5.1	303	2	T32277	hypothetical prote	615	71	5.1	469	2	E86075	probable permease
543	71.5	5.1	308	2	H70767	hypothetical prote	616	71	5.1	478	2	A97079	MDR-type permease
544	71.5	5.1	323	2	G84003	DNA transport mach	617	71	5.1	492	2	D75188	proline symporter
545	71.5	5.1	324	2	F81018	iron(III) ABC tran	618	71	5.1	502	2	H81796	NADH2 dehydrogenas
546	71.5	5.1	337	2	F82214	galactoside ABC tr	619	71	5.1	502	1	ACHU47	nicotinic acetylch
547	71.5	5.1	341	2	F82712	integral membrane	620	71	5.1	502	2	G02259	alpha 7 neuronal n
548	71.5	5.1	348	2	A82322	octaprenyl-diphosp	621	71	5.1	502	2	A57175	nicotinic acetylch
549	71.5	5.1	349	2	T31856	hypothetical prote	622	71	5.1	502	2	T101378	nicotinic receptor
550	71.5	5.1	373	2	A98094	type III secretion	623	71	5.1	509	2	A82840	beta-lactamase ind
551	71.5	5.1	373	2	E85939	hypothetical prote	624	71	5.1	541	2	D82302	iron(III) ABC tran
552	71.5	5.1	373	2	D71142	hypothetical prote	625	71	5.1	555	2	T24671	hypothetical prote
553	71.5	5.1	382	2	H85014	probable acetyltra	626	71	5.1	569	2	T00477	probable amino aci
554	71.5	5.1	391	2	A55119	potassium channel	627	71	5.1	579	2	AB1414	ABC transporter (A
555	71.5	5.1	406	2	C86904	transporter yxbD [628	71	5.1	593	2	AI0559	probable ABC trans
556	71.5	5.1	418	2	H97763	proline/betaine tr	629	71	5.1	594	2	A49804	cellular Hsp70 hom
557	71.5	5.1	432	2	D95369	conserved hypothet	630	71	5.1	612	2	S74936	sulfur deprivation
558	71.5	5.1	445	2	T20190	hypothetical prote	631	71	5.1	684	2	T12151	NADH2 dehydrogenas
559	71.5	5.1	470	2	A69751	histidine permease	632	71	5.1	685	2	T12138	NADH2 dehydrogenas
560	71.5	5.1	470	2	C70554	hypothetical prote	633	71	5.1	686	2	T12128	NADH2 dehydrogenas
561	71.5	5.1	477	2	F86670	lysine specific pe	634	71	5.1	688	2	T13237	NADH2 dehydrogenas
562	71.5	5.1	497	2	G81598	serine hydroxymeth	635	71	5.1	688	2	T13249	NADH2 dehydrogenas
563	71.5	5.1	506	2	F88934	protein K04F1.14 [636	71	5.1	698	2	T12560	NADH2 dehydrogenas
564	71.5	5.1	512	2	S75887	hypothetical prote	637	71	5.1	699	2	T12648	NADH2 dehydrogenas
565	71.5	5.1	519	2	E86555	serine hydroxymeth	638	71	5.1	704	2	T13729	NADH2 dehydrogenas
566	71.5	5.1	519	2	H72067	glycine hydroxymet	639	71	5.1	737	2	T13067	NADH2 dehydrogenas
567	71.5	5.1	532	2	S59087	cytochrome-c oxida	640	71	5.1	918	2	A36337	membrane glycoprot
568	71.5	5.1	532	2	S86087	amino acid transpo	641	71	5.1	1506	2	T51900	related to PAN2 pr
569	71.5	5.1	533	2	H69326	conserved hypothet	642	70.5	5.1	133	2	A13582	hypothetical prote
570	71.5	5.1	534	2	C87023	probable cell divi	643	70.5	5.1	167	2	T20548	hypothetical prote
571	71.5	5.1	539	2	S77595	cytochrome-c oxida	644	70.5	5.1	175	2	T39999	hypothetical prote
572	71.5	5.1	654	2	H89871	hypothetical prote	645	70.5	5.1	210	2	F64609	conserved hypothet
573	71.5	5.1	663	2	AG2696	cytochrome c-type	646	70.5	5.1	214	2	S76538	hypothetical prote
574	71.5	5.1	663	2	G97478	cytochrome c-type	647	70.5	5.1	227	2	C64815	ybM protein - Esc
575	71.5	5.1	665	2	B96668	probable acyl-CoA	648	70.5	5.1	253	2	F75067	hypothetical prote
576	71.5	5.1	672	2	AF3084	conserved hypothet	649	70.5	5.1	263	2	T29414	hypothetical prote
577	71.5	5.1	672	2	C98202	hypothetical prote	650	70.5	5.1	263	2	T04051	hypothetical prote
578	71.5	5.1	695	2	B87265	Kup system potaasi	651	70.5	5.1	267	2	H72590	hypothetical prote
579	71.5	5.1	698	2	T12590	NADH2 dehydrogenas	652	70.5	5.1	285	2	D87209	probable plasma me
580	71.5	5.1	718	1	B64040	hypothetical prote	653	70.5	5.1	285	2	T02451	probable transmemb
581	71.5	5.1	730	2	T12224	NADH2 dehydrogenas	654	70.5	5.1	286	2	T02451	plasma membrane in
582	71.5	5.1	741	2	T12642	NADH2 dehydrogenas	655	70.5	5.1	288	2	S41194	transmembrane prot
583	71.5	5.1	741	2	T12701	NADH2 dehydrogenas	656	70.5	5.1	290	2	A69779	conserved hypothet
584	71.5	5.1	746	2	T13678	NADH2 dehydrogenas	657	70.5	5.1	297	2	G69357	hypothetical prote
585	71.5	5.1	755	2	T04187	subtilisin-like pr	658	70.5	5.1	312	2	AB0306	probable membrane
586	71.5	5.1	765	2	F73186	probable cell wall	659	70.5	5.1	315	1	C69763	ferrichrome ABC tr
587	71.5	5.1	770	2	T23999	hypothetical prote	660	70.5	5.1	315	2	C81862	probable inner mem
588	71.5	5.1	854	2	D82324	conserved hypothet	661	70.5	5.1	318	2	E71054	probable sodium de
589	71.5	5.1	1067	2	AB0260	probable phage hos	662	70.5	5.1	327	2	D75196	hypothetical prote
590	71.5	5.1	1679	2	T50091	yeast Ecm29 cell w	663	70.5	5.1	346	2	AB0187	probable iron-side
591	71	5.1	200	1	F45456	NADH2 dehydrogenas	664	70.5	5.1	349	2	T33948	hypothetical prote
592	71	5.1	228	2	AE2541	hypothetical prote	665	70.5	5.1	358	2	T22823	hypothetical prote
593	71	5.1	229	2	A64137	molybdenum transpo	666	70.5	5.1	386	2	E69765	branched chain ami
594	71	5.1	243	2	B86740	lipopolysaccharide	667	70.5	5.1	387	2	AE1062	hypothetical prote
595	71	5.1	260	2	T30669	probable trans-act	668	70.5	5.1	394	2	C81333	probable efflux pu
596	71	5.1	260	2	C82116	flagellar biosynth	669	70.5	5.1	408	2	B42290	probable membrane
597	71	5.1	261	2	H92217	hypothetical prote	670	70.5	5.1	419	2	B90033	hypothetical prote
598	71	5.1	272	2	T11689	NADH2 dehydrogenas	671	70.5	5.1	430	2	A95935	conserved hypothet
599	71	5.1	297	2	AD2318	transcription regu	672	70.5	5.1	434	2	T15799	hypothetical prote
600	71	5.1	305	2	E90461	hypothetical prote	673	70.5	5.1	443	2	D71058	hypothetical prote
601	71	5.1	316	2	AB2931	hypothetical prote	674	70.5	5.1	446	2	B99284	conserved hypothet
602	71	5.1	316	2	D98351	dipeptide ABC tran	675	70.5	5.1	457	2	A83677	sodium-dependent t
603	71	5.1	333	2	T41689	hypothetical prote	676	70.5	5.1	458	2	B90615	NADH dehydrogenase
604	71	5.1	364	2	H83787	hypothetical prote	677	70.5	5.1	474	2	T38737	probable CAXX pren
605	71	5.1	396	1	E64143	chloramphenicol re	678	70.5	5.1	480	2	S39978	scrA protein - Sta
606	71	5.1	397	2	C95221	hypothetical prote	679	70.5	5.1	491	2	AC1499	transmembrane prot
607	71	5.1	397	2	T00098	hypothetical prote	680	70.5	5.1	507	2	AB1707	glycine betaine tr
608	71	5.1	397	2	B98085	hypothetical prote	681	70.5	5.1	507	2	B64433	probable O-antigen
609	71	5.1	448	2	T30982	hypothetical prote	682	70.5	5.1	508	2	D81325	probable phosphate
610	71	5.1	458	2	AF0631	probable 4-hydroxy	683	70.5	5.1	533	2	S51171	amino acid transpo
611	71	5.1	461	2	S60253	sel-12 protein - C	684	70.5	5.1	585	2	C82955	probable sodium/pr
612	71	5.1	466	2	E90046	hypothetical prote	685	70.5	5.1	593	2	JT0374	cytochrome-c oxida
613	71	5.1	468	2	I64182	Na+/H+-exchanging	686	70.5	5.1	593	2	F84223	cytochrome-c oxida

687	70.5	5.1	674	2	AC1913	two-component sens	760	70	5.0	2201	1	GNNYA9	genome polyprotein
688	70.5	5.1	683	2	T12158	NADH2 dehydrogenas	761	69.5	5.0	202	2	F86347	hypothetical prote
689	70.5	5.1	704	2	T13581	NADH2 dehydrogenas	762	69.5	5.0	210	2	H81406	probable integral
690	70.5	5.1	718	2	S48726	phenylalanine ammo	763	69.5	5.0	215	2	S75345	hypothetical prote
691	70.5	5.1	733	2	T12213	NADH2 dehydrogenas	764	69.5	5.0	222	2	E72228	hypothetical prote
692	70.5	5.1	737	2	T13504	NADH2 dehydrogenas	765	69.5	5.0	224	2	B71191	hypothetical prote
693	70.5	5.1	738	2	C95936	conserved hypotet	766	69.5	5.0	256	2	S26742	tonoplast intrinsi
694	70.5	5.1	740	1	DENTN5	NADH2 dehydrogenas	767	69.5	5.0	260	2	G64690	type IIS restricti
695	70.5	5.1	741	2	T12610	NADH2 dehydrogenas	768	69.5	5.0	265	2	AF2007	hypothetical prote
696	70.5	5.1	741	2	T12702	NADH2 dehydrogenas	769	69.5	5.0	268	2	A70417	hypothetical prote
697	70.5	5.1	741	2	T13233	NADH2 dehydrogenas	770	69.5	5.0	285	1	C32804	prephenate dehydra
698	70.5	5.1	741	2	T13569	NADH2 dehydrogenas	771	69.5	5.0	285	2	AE1488	Staphylococcus xyl
699	70.5	5.1	921	2	T19694	hypothetical prote	772	69.5	5.0	286	2	F87075	membrane transpor
700	70.5	5.1	1134	2	A41350	adenylate cyclase	773	69.5	5.0	287	2	T09791	drought-induced ma
701	70.5	5.1	1681	2	A55138	sodium channel mNa	774	69.5	5.0	292	2	S75288	hypothetical prote
702	70.5	5.1	1781	1	A34374	DNA-directed RNA p	775	69.5	5.0	294	2	S76277	ycf38 protein - Sy
703	70.5	5.1	2143	2	G96595	hypothetical prote	776	69.5	5.0	308	2	S16648	dispeptide transpor
704	70	5.0	98	2	T17099	NADH2 dehydrogenas	777	69.5	5.0	315	2	F72374	conserved hypotet
705	70	5.0	160	2	F72322	hypothetical prote	778	69.5	5.0	317	2	S72851	hypothetical prote
706	70	5.0	169	2	F72329	acetyltransferase	779	69.5	5.0	325	2	T14227	NADH2 dehydrogenas
707	70	5.0	209	2	H97519	hypothetical prote	780	69.5	5.0	329	2	T11350	NADH2 dehydrogenas
708	70	5.0	240	1	Q0B5G3	HwLF4 protein - hu	781	69.5	5.0	334	2	T13955	hypothetical prote
709	70	5.0	245	2	A90527	hypothetical prote	782	69.5	5.0	340	2	AE0353	probable membrane
710	70	5.0	250	2	C91020	hypothetical prote	783	69.5	5.0	351	2	T11794	NADH2 dehydrogenas
711	70	5.0	251	2	AH0575	2,3-dihydro-2,3-di	784	69.5	5.0	353	2	S65297	probable membrane
712	70	5.0	254	2	B70235	hypothetical prote	785	69.5	5.0	358	2	T29744	hypothetical prote
713	70	5.0	273	2	A72378	conserved hypotet	786	69.5	5.0	371	2	H97452	cytochrome c oxida
714	70	5.0	282	2	A99205	hypothetical prote	787	69.5	5.0	372	2	G82790	hypothetical prote
715	70	5.0	287	2	T12440	mipC protein - com	788	69.5	5.0	385	2	AE2717	permease [imported
716	70	5.0	320	2	T20176	hypothetical prote	789	69.5	5.0	385	2	H97498	permease AGR_C 211
717	70	5.0	325	2	C98135	hypothetical prote	790	69.5	5.0	393	1	A48357	nonstructural prot
718	70	5.0	325	2	AH3152	hypothetical prote	791	69.5	5.0	398	2	C90349	multidrug-efflux t
719	70	5.0	344	2	AE3228	agrocinopine synth	792	69.5	5.0	415	2	A39412	tryptophan transpo
720	70	5.0	345	2	S51948	hypothetical prote	793	69.5	5.0	420	2	A12458	hypothetical prote
721	70	5.0	397	2	H95381	probable iron upta	794	69.5	5.0	426	2	E86575	phosphate permease
722	70	5.0	413	2	H81659	hypothetical prote	795	69.5	5.0	439	2	A64769	branched-chain ami
723	70	5.0	427	2	S74444	hypothetical prote	796	69.5	5.0	439	2	C90685	branched-chain ami
724	70	5.0	442	2	E85864	probable transport	797	69.5	5.0	439	2	G85535	branched-chain ami
725	70	5.0	443	2	H85485	probable transport	798	69.5	5.0	440	2	H90253	NADH-Ubiquinone/pl
726	70	5.0	443	2	H90634	probable transport	799	69.5	5.0	443	2	AG1335	hypothetical prote
727	70	5.0	456	2	F97810	magnesium transpor	800	69.5	5.0	448	2	A69747	ABC transporter (p
728	70	5.0	458	2	A37869	alpha-2B-adrenergi	801	69.5	5.0	458	2	B81409	probable transmemb
729	70	5.0	459	2	T11110	NADH2 dehydrogenas	802	69.5	5.0	459	2	S10196	NADH2 dehydrogenas
730	70	5.0	459	2	S28025	light harvesting c	803	69.5	5.0	470	2	C87683	conserved hypotet
731	70	5.0	467	2	F91228	probable permease	804	69.5	5.0	472	2	B91091	l-arabinose isomer
732	70	5.0	503	2	AB2734	NADH dehydrogenase	805	69.5	5.0	472	2	E85936	l-arabinose isomer
733	70	5.0	503	2	D97515	NADH dehydrogenase	806	69.5	5.0	472	2	B26430	cytochrome-c oxida
734	70	5.0	519	2	F84222	quinone oxidoreduc	807	69.5	5.0	475	2	E83450	cytochrome-c oxida
735	70	5.0	522	2	B83987	ABC transporter (p	808	69.5	5.0	475	2	D83128	NADH2 dehydrogenas
736	70	5.0	539	2	E97025	spoVB related memb	809	69.5	5.0	478	2	AC3395	NADH2 dehydrogenas
737	70	5.0	539	2	S67049	probable membrane	810	69.5	5.0	482	2	T45295	cytochrome-c oxida
738	70	5.0	576	2	B71420	hypothetical prote	811	69.5	5.0	493	2	S52421	amino acid transpo
739	70	5.0	600	2	T32343	hypothetical prote	812	69.5	5.0	507	2	T48645	glycine betaine tr
740	70	5.0	614	2	B84949	NADH2 dehydrogenas	813	69.5	5.0	507	2	AD1336	glycine betaine tr
741	70	5.0	658	2	B86599	metal transport p-	814	69.5	5.0	515	2	T03717	GTP-binding protei
742	70	5.0	658	2	D72026	metal transport p-	815	69.5	5.0	536	2	A71491	probable integral
743	70	5.0	670	2	JQ1447	NADH2 dehydrogenas	816	69.5	5.0	536	2	S42708	proline transport
744	70	5.0	683	2	C81515	cation-transportin	817	69.5	5.0	570	2	S04547	proline transport
745	70	5.0	683	2	T12556	NADH2 dehydrogenas	818	69.5	5.0	572	2	AB2671	cytochrome-c oxida
746	70	5.0	688	2	T12670	NADH2 dehydrogenas	819	69.5	5.0	591	2	S14115	NADH2 dehydrogenas
747	70	5.0	698	2	T12556	NADH2 dehydrogenas	820	69.5	5.0	591	2	S43506	hypothetical prote
748	70	5.0	700	2	T13702	NADH2 dehydrogenas	821	69.5	5.0	615	2	S77332	NADH2 dehydrogenas
749	70	5.0	705	2	T13494	NADH2 dehydrogenas	822	69.5	5.0	627	2	T11125	NADH2 dehydrogenas
750	70	5.0	732	2	T12194	NADH2 dehydrogenas	823	69.5	5.0	627	2	S67257	proline transport
751	70	5.0	738	2	T14230	exodeoxyribonuclea	824	69.5	5.0	631	2	S75742	hypothetical prote
752	70	5.0	744	2	A81719	hypothetical prote	825	69.5	5.0	643	2	S70592	NADH2 dehydrogenas
753	70	5.0	782	2	T25925	protein F35H12.3 [826	69.5	5.0	654	2	T14202	NADH2 dehydrogenas
754	70	5.0	836	2	E89453	adenylate cyclase	827	69.5	5.0	686	2	T13680	NADH2 dehydrogenas
755	70	5.0	860	2	AB2044	hypothetical prote	828	69.5	5.0	701	2	T12296	NADH2 dehydrogenas
756	70	5.0	1018	2	T19693	probable arabinosy	829	69.5	5.0	718	2	A99195	hypothetical prote
757	70	5.0	1070	2	B86922	hypothetical prote	830	69.5	5.0	736	2	T12214	NADH2 dehydrogenas
758	70	5.0	1155	2	B71720	hypothetical prote	831	69.5	5.0	741	2	T12706	NADH2 dehydrogenas
759	70	5.0	2108	2	S72458	sodium channel pro	832	69.5	5.0	741	2	T13086	NADH2 dehydrogenas

833	69.5	5.0	741	2	T13372	NADH2 dehydrogenas	906	69	5.0	1	DNORUB	NADH2 dehydrogenas	
834	69.5	5.0	744	2	T13682	NADH2 dehydrogenas	907	69	5.0	677	2	T11231	NADH2 dehydrogenas
835	69.5	5.0	747	2	E91049	probable cytochrom	908	69	5.0	684	2	T13695	NADH2 dehydrogenas
836	69.5	5.0	747	2	A85894	probable cytochrom	909	69	5.0	691	2	T12293	probable thiol-dis
837	69.5	5.0	809	1	SYBYQT	glutamine-tRNA lig	910	69	5.0	692	2	H71494	NADH2 dehydrogenas
838	69.5	5.0	970	2	A13605	potassium efflux s	911	69	5.0	702	2	T13505	hypothetical prote
839	69.5	5.0	1302	2	B41249	multidrug resistanc	912	69	5.0	724	2	B83342	NADH2 dehydrogenas
840	69.5	5.0	1645	2	T31339	carbamoyl-phosphat	913	69	5.0	737	2	T12193	NADH2 dehydrogenas
841	69.5	5.0	1827	2	A35694	cut1 protein - fis	914	69	5.0	777	2	AF2410	serine/threonine k
842	69.5	5.0	1828	2	T41455	cut1 protein - fis	915	69	5.0	903	2	AI0015	maltoase regulon po
843	69	5.0	139	2	T31033	hypothetical prote	916	69	5.0	904	2	A84212	hypothetical prote
844	69	5.0	171	2	AF2434	hypothetical prote	917	69	5.0	975	2	T22788	hypothetical prote
845	69	5.0	233	2	S77443	cytochrome-c oxida	918	68.5	4.9	179	2	AD2573	hypothetical prote
846	69	5.0	233	2	AH1068	probable membrane	919	68.5	4.9	212	2	AE1473	hypothetical prote
847	69	5.0	236	2	S42069	TSGT protein - rat	920	68.5	4.9	278	2	T11550	probable membrane
848	69	5.0	254	2	C84315	hypothetical prote	921	68.5	4.9	289	2	D87933	protein R06C1.2 [i
849	69	5.0	260	2	AG0434	probable membrane	922	68.5	4.9	295	2	T01528	probable plasma me
850	69	5.0	281	2	D64426	phosphate transpor	923	68.5	4.9	296	2	B69025	conserved hypothet
851	69	5.0	288	2	H72092	prolipoprotein dia	924	68.5	4.9	303	2	AG1396	cation transport p
852	69	5.0	288	2	G86529	prolipoprotein dia	925	68.5	4.9	305	2	S66005	conserved hypothet
853	69	5.0	290	2	T09260	aquaporin-like tra	926	68.5	4.9	313	2	C71545	probable oligopept
854	69	5.0	292	2	D81575	prolipoprotein dia	927	68.5	4.9	333	2	S52960	NADH2 dehydrogenas
855	69	5.0	296	1	BVECF7	phosphate transpor	928	68.5	4.9	336	2	I64096	transmembrane pore
856	69	5.0	296	2	F91211	hypothetical prote	929	68.5	4.9	346	2	B98135	hypothetical prote
857	69	5.0	296	2	F86057	hypothetical prote	930	68.5	4.9	346	2	AI3152	hypothetical prote
858	69	5.0	299	2	T06960	probable membrane	931	68.5	4.9	347	2	G96741	unknown protein F1
859	69	5.0	305	2	F70030	conserved hypothet	932	68.5	4.9	352	2	T23962	hypothetical prote
860	69	5.0	308	2	C86561	phosphatidate cyti	933	68.5	4.9	365	2	C97088	spore germination
861	69	5.0	308	2	H72062	phosphatidate cyti	934	68.5	4.9	367	2	T14228	NADH2 dehydrogenas
862	69	5.0	313	2	H71341	conserved hypothet	935	68.5	4.9	372	2	AB0276	probable membrane
863	69	5.0	347	2	T29415	hypothetical prote	936	68.5	4.9	383	2	C83436	probable MFS metab
864	69	5.0	364	2	D96973	spore germination	937	68.5	4.9	401	2	G95968	probable transport
865	69	5.0	369	2	F69478	NADH2 dehydrogenas	938	68.5	4.9	407	2	A69188	ammonium transport
866	69	5.0	387	2	E83679	multidrug-efflux t	939	68.5	4.9	454	2	AE1244	acetyl-CoA carboxy
867	69	5.0	389	2	T51355	membrane protein [940	68.5	4.9	454	2	AI1606	acetyl-CoA carboxy
868	69	5.0	391	2	AB1285	transmembrane tran	941	68.5	4.9	455	2	F97065	D-xylose-transport sy
869	69	5.0	396	2	F83110	probable MFS trans	942	68.5	4.9	459	2	B95009	potassium uptake p
870	69	5.0	397	2	B81223	conserved hypothet	943	68.5	4.9	459	2	F97880	hypothetical prote
871	69	5.0	397	2	B81994	probable transmemb	944	68.5	4.9	459	2	H81952	probable integral
872	69	5.0	411	2	F97088	sugar-proton sympo	945	68.5	4.9	468	2	AP2163	hypothetical prote
873	69	5.0	416	2	C81324	ubiquinol-cytochro	946	68.5	4.9	475	2	C83452	cytochrome-c oxida
874	69	5.0	429	2	AI0792	probable transport	947	68.5	4.9	487	2	E97747	NADH2 dehydrogenas
875	69	5.0	431	2	A84380	hypothetical prote	948	68.5	4.9	488	1	QXASB1	mRNA maturase b11
876	69	5.0	432	2	C85087	hypothetical prote	949	68.5	4.9	489	2	E89102	DNA gyrase, subuni
877	69	5.0	443	2	E64725	yaaU protein - Esc	950	68.5	4.9	507	2	B69316	probable WD-domain
878	69	5.0	449	2	AE1707	PIS system galacti	951	68.5	4.9	509	2	T41034	probable transport
879	69	5.0	451	2	E81781	probable integral	952	68.5	4.9	537	2	AI1277	hypothetical prote
880	69	5.0	451	2	A81206	sugar transporter,	953	68.5	4.9	546	2	G86440	hypothetical prote
881	69	5.0	455	2	B90619	NADH dehydrogenase	954	68.5	4.9	597	2	T41501	major facilitator
882	69	5.0	458	2	B96643	hypothetical prote	955	68.5	4.9	616	2	F90371	amino acid transpo
883	69	5.0	462	2	D86814	transport protein	956	68.5	4.9	627	2	C96981	ABC transporter AT
884	69	5.0	464	2	C40630	GDP-mannose pyroph	957	68.5	4.9	637	2	AC3217	potassium uptake p
885	69	5.0	473	2	T03611	cyclin, B-type - c	958	68.5	4.9	685	2	T12129	NADH2 dehydrogenas
886	69	5.0	478	2	T29174	hypothetical prote	959	68.5	4.9	687	2	T12126	NADH2 dehydrogenas
887	69	5.0	482	2	C90067	hypothetical prote	960	68.5	4.9	688	2	T13242	NADH2 dehydrogenas
888	69	5.0	483	2	A81352	integral membrane	961	68.5	4.9	688	2	T13373	NADH2 dehydrogenas
889	69	5.0	487	2	S40820	probable permease	962	68.5	4.9	689	2	T13681	NADH2 dehydrogenas
890	69	5.0	488	1	H64537	cytochrome-c oxida	963	68.5	4.9	698	2	T13492	NADH2 dehydrogenas
891	69	5.0	488	2	G71969	cytochrome-c oxida	964	68.5	4.9	701	2	F70155	Na+/H+ antiporter
892	69	5.0	492	2	AD3055	succinoglycan bios	965	68.5	4.9	716	2	B80216	probable integral
893	69	5.0	495	2	S75340	NADH2 dehydrogenas	966	68.5	4.9	721	2	B83820	hypothetical prote
894	69	5.0	498	2	H82494	probable NADH dehy	967	68.5	4.9	736	2	T12225	NADH2 dehydrogenas
895	69	5.0	509	2	D86978	hypothetical prote	968	68.5	4.9	736	2	T12222	NADH2 dehydrogenas
896	69	5.0	516	2	G82182	probable NADH dehy	969	68.5	4.9	741	2	T12711	NADH2 dehydrogenas
897	69	5.0	522	2	A98231	succinoglycan bios	970	68.5	4.9	741	2	T12620	NADH2 dehydrogenas
898	69	5.0	528	2	T34941	probable Na+/H+ an	971	68.5	4.9	741	2	T12699	NADH2 dehydrogenas
899	69	5.0	554	2	S03809	cytochrome-c oxida	972	68.5	4.9	743	2	T13700	NADH2 dehydrogenas
900	69	5.0	588	2	A43740	DG42 protein - Afr	973	68.5	4.9	743	2	T12760	NADH2 dehydrogenas
901	69	5.0	591	2	G97748	virD4 protein [imp	974	68.5	4.9	744	2	T12705	NADH2 dehydrogenas
902	69	5.0	605	2	H95240	conserved hypothet	975	68.5	4.9	745	2	G84995	vacB protein [imp
903	69	5.0	605	2	A99705	hypothetical prote	976	68.5	4.9	746	2	C95110	competence protein
904	69	5.0	642	2	T33262	hypothetical prote	977	68.5	4.9	747	2	T13683	NADH2 dehydrogenas
905	69	5.0	652	2	C97087	probable permease	978	68.5	4.9	750	2	B90137	sulfate permease [

979	68.5	4.9	820	2	D71471	probable DNA misma	1052	68	4.9	899	2	S76449	hypothetical prote
980	68.5	4.9	827	2	A95877	hypothetical prote	1053	68	4.9	906	2	S35342	Golgi-associated p
981	68.5	4.9	870	2	A89201	protein F32D8.4 [i	1054	68	4.9	999	2	F72453	probable cytochrom
982	68.5	4.9	874	2	Q00883	genome polypeptid	1055	68	4.9	1039	2	C87083	C-term lysyl-tRNA
983	68.5	4.9	881	2	AE2777	potassium efflux s	1056	68	4.9	1082	2	T45096	probable arabinosy
984	68.5	4.9	881	2	B97557	hypothetical prote	1057	68	4.9	1323	2	T18214	ATP binding casses
985	68.5	4.9	912	2	T21659	hypothetical prote	1058	68	4.9	1368	2	S71622	probable aldehyde
986	68.5	4.9	960	2	A82142	probable cell divi	1059	68	4.9	1541	1	S71839	canalicular multidi
987	68.5	4.9	1081	2	T52028	cellulose synthase	1060	67.5	4.8	100	2	B69836	hypothetical prote
988	68.5	4.9	1084	2	T08583	cellulose synthase	1061	67.5	4.8	212	2	A11111	hypothetical prote
989	68.5	4.9	1394	2	S66876	ATP-dependent tran	1062	67.5	4.8	269	2	E72693	hypothetical prote
990	68.5	4.9	1504	2	A33602	DNA-directed DNA p	1063	67.5	4.8	284	2	A11198	Streptococcus agal
991	68	4.9	148	2	S74589	hypothetical prote	1064	67.5	4.8	288	2	T33224	hypothetical prote
992	68	4.9	183	2	T49855	hypothetical prote	1065	67.5	4.8	291	2	B95316	probable ABC trans
993	68	4.9	214	2	G83882	hypothetical prote	1066	67.5	4.8	293	2	D81673	ABC transporter, p
994	68	4.9	215	2	S16564	noIH protein - Rhi	1067	67.5	4.8	300	2	G70943	hypothetical prote
995	68	4.9	237	2	H86841	transport permease	1068	67.5	4.8	302	2	G90078	hypothetical prote
996	68	4.9	241	2	T33804	hypothetical prote	1069	67.5	4.8	302	2	G71660	hypothetical prote
997	68	4.9	252	2	A70529	hypothetical prote	1070	67.5	4.8	302	2	AF2686	ABC transporter, m
998	68	4.9	254	2	E70438	type 4 prepilin pe	1071	67.5	4.8	302	2	C97468	probable permease
999	68	4.9	256	2	C72261	spermidine/putresc	1072	67.5	4.8	304	2	AD1029	probable membrane
1000	68	4.9	265	2	AD0214	PTS system, mannose	1073	67.5	4.8	307	2	C70952	probable sugA prot
1001	68	4.9	265	2	E82716	ATP synthase, A ch	1074	67.5	4.8	310	2	A86812	sugar ABC transport
1002	68	4.9	282	2	AD0848	iron transport pro	1075	67.5	4.8	314	2	AB2230	hypothetical prote
1003	68	4.9	286	2	D83914	chloramphenicol re	1076	67.5	4.8	323	2	T31828	hypothetical prote
1004	68	4.9	296	2	AD0956	phosphate transpor	1077	67.5	4.8	327	1	S45529	NADPH2:quinone red
1005	68	4.9	304	2	A89005	hypothetical prote	1078	67.5	4.8	327	2	S67168	probable membrane
1006	68	4.9	312	2	F70044	hypothetical prote	1079	67.5	4.8	344	2	T32600	hypothetical prote
1007	68	4.9	316	2	S50336	NADH2 dehydrogenas	1080	67.5	4.8	347	2	T28733	hypothetical prote
1008	68	4.9	316	2	E81321	probable cation tr	1081	67.5	4.8	349	2	S51267	probable galactosy
1009	68	4.9	329	2	F98334	SN-glycerol 3-phos	1082	67.5	4.8	359	2	I51372	angiotensin II rec
1010	68	4.9	335	2	S44635	F22b7.7 protein -	1083	67.5	4.8	361	2	D72384	conserved hypoteth
1011	68	4.9	353	2	T06515	probable adenosylm	1084	67.5	4.8	364	1	S77360	cbid protein - Syn
1012	68	4.9	357	2	C97744	hypothetical prote	1085	67.5	4.8	367	2	T23290	hypothetical prote
1013	68	4.9	358	2	T38914	para-hydroxybenzoa	1086	67.5	4.8	374	2	C91198	EspD protein limpo
1014	68	4.9	396	2	AF0677	probable antibioti	1087	67.5	4.8	374	2	G86044	secreted protein E
1015	68	4.9	396	2	A91019	probable antibioti	1088	67.5	4.8	377	2	T21170	hypothetical prote
1016	68	4.9	396	2	C85863	probable antibioti	1089	67.5	4.8	379	2	D81515	cell shape-determi
1017	68	4.9	397	2	G90013	hypothetical prote	1090	67.5	4.8	387	2	JE0364	lactosylceramide a
1018	68	4.9	408	2	AC1373	conserved hypoteth	1091	67.5	4.8	393	2	T12608	NADH2 dehydrogenas
1019	68	4.9	417	2	B82966	tryptophan permeas	1092	67.5	4.8	402	2	B69843	conserved hypoteth
1020	68	4.9	437	1	F64614	conserved hypoteth	1093	67.5	4.8	409	2	AF3271	probable allantoin
1021	68	4.9	442	2	H81402	probable integral	1094	67.5	4.8	415	2	F91209	low affinity trypt
1022	68	4.9	448	2	G70172	conserved hypoteth	1095	67.5	4.8	415	2	A86056	low affinity trypt
1023	68	4.9	461	2	H82186	probable multidrug	1096	67.5	4.8	415	2	A86599	rod shape protein
1024	68	4.9	469	2	C69628	gamma-aminobutyra	1097	67.5	4.8	415	2	C72026	rod shape protein
1025	68	4.9	476	2	D83600	probable aldehyde	1098	67.5	4.8	415	2	H71841	hypothetical prote
1026	68	4.9	485	2	T24115	hypothetical prote	1099	67.5	4.8	426	2	A96000	probable C4-dicarb
1027	68	4.9	488	1	OXASN4	NADH2 dehydrogenas	1100	67.5	4.8	456	2	B83391	probable amino aci
1028	68	4.9	489	2	B53153	glucose transport	1101	67.5	4.8	456	2	E83750	glucuronate permease
1029	68	4.9	494	2	JC2382	sodium/proline sym	1102	67.5	4.8	459	2	S47879	NADH2 dehydrogenas
1030	68	4.9	505	2	B97747	NADH2 dehydrogenas	1103	67.5	4.8	462	2	D81010	conserved hypoteth
1031	68	4.9	512	2	G90399	amino acid transpo	1104	67.5	4.8	463	2	A69905	probable adenylate
1032	68	4.9	521	2	B64181	probable cytochrom	1105	67.5	4.8	463	2	E83242	hypothetical prote
1033	68	4.9	523	2	T12198	sucrose transport	1106	67.5	4.8	467	2	AB2493	hypothetical prote
1034	68	4.9	534	2	S64593	probable membrane	1107	67.5	4.8	467	2	A81263	probable integral
1035	68	4.9	537	2	AH1640	probable transport	1108	67.5	4.8	477	2	D83617	probable amino aci
1036	68	4.9	550	2	T37519	probable amino aci	1109	67.5	4.8	483	2	A10449	protein-Npi-phosph
1037	68	4.9	564	2	C83742	cytochrome c oxida	1110	67.5	4.8	486	2	F71683	NADH2 dehydrogenas
1038	68	4.9	592	2	E70488	cytochrome-c oxida	1111	67.5	4.8	490	2	E82740	C4-dicarboxylate t
1039	68	4.9	593	2	S26696	alkaline proteinase	1112	67.5	4.8	495	2	B81297	sodium/proline sym
1040	68	4.9	600	2	C69371	conserved hypoteth	1113	67.5	4.8	501	2	T02134	hypothetical prote
1041	68	4.9	602	2	T13679	NADH2 dehydrogenas	1114	67.5	4.8	510	2	H87320	conserved hypoteth
1042	68	4.9	617	2	F82744	ferrous iron trans	1115	67.5	4.8	512	2	S28663	cytochrome-c oxida
1043	68	4.9	633	2	I58140	glycine transporte	1116	67.5	4.8	513	2	I45456	NADH2 dehydrogenas
1044	68	4.9	633	2	S45877	uracil transport p	1117	67.5	4.8	514	2	T46131	4-coumarate-CoA 11
1045	68	4.9	638	2	JH0673	glycine transport	1118	67.5	4.8	519	1	S02153	NADH2 dehydrogenas
1046	68	4.9	683	2	T12295	NADH2 dehydrogenas	1119	67.5	4.8	552	2	E70731	probable pitB prot
1047	68	4.9	688	2	T13278	NADH2 dehydrogenas	1120	67.5	4.8	560	2	F81423	L-lactate permease
1048	68	4.9	689	2	T13762	NADH2 dehydrogenas	1121	67.5	4.8	568	2	JC7911	Na+-coupled citrat
1049	68	4.9	705	2	T12152	NADH2 dehydrogenas	1122	67.5	4.8	615	2	H82635	hypothetical prote
1050	68	4.9	709	2	A97218	uncharacterized co	1123	67.5	4.8	617	2	B82285	protein-export mem
1051	68	4.9	811	2	T36591	probable transmem	1124	67.5	4.8	631	2	H70754	probable abc trans

1125	67.5	4.8	637	2	JH0674	L-proline transpor	1198	67	4.8	406	2	H89006	protein T22F3.11 [
1126	67.5	4.8	645	2	T12159	NADH2 dehydrogenas	1199	67	4.8	407	2	AD0706	O-antigen polymera
1127	67.5	4.8	645	2	A75390	NADH2 dehydrogenas	1200	67	4.8	407	2	A43672	O-antigen polymera
1128	67.5	4.8	659	2	T33557	hypothetical prote	1201	67	4.8	409	2	C82644	transcription regu
1129	67.5	4.8	690	2	D75487	v-type ATP synthas	1202	67	4.8	411	2	S61245	glucosyl transfe
1130	67.5	4.8	699	2	T12169	NADH2 dehydrogenas	1203	67	4.8	416	2	JN0720	hypothetical prote
1131	67.5	4.8	703	2	T13074	NADH2 dehydrogenas	1204	67	4.8	417	2	H83708	hypothetical prote
1132	67.5	4.8	741	2	T13404	NADH2 dehydrogenas	1205	67	4.8	421	2	AF2382	hypothetical prote
1133	67.5	4.8	741	2	T133760	NADH2 dehydrogenas	1206	67	4.8	423	2	E82611	conserved hypochet
1134	67.5	4.8	741	2	T13776	NADH2 dehydrogenas	1207	67	4.8	430	2	S74039	hypothetical prote
1135	67.5	4.8	741	2	T12762	NADH2 dehydrogenas	1208	67	4.8	446	2	AC3349	protein translocas
1136	67.5	4.8	744	2	T12694	NADH2 dehydrogenas	1209	67	4.8	453	2	A43765	stsl+ protein - fi
1137	67.5	4.8	744	2	T12611	NADH2 dehydrogenas	1210	67	4.8	453	2	T30985	hypothetical prote
1138	67.5	4.8	801	2	A98862	Na+/H+ antiporter	1211	67	4.8	456	2	A12789	manganese transpor
1139	67.5	4.8	812	2	T19446	hypothetical prote	1212	67	4.8	458	2	H17657	NADH2 dehydrogenas
1140	67.5	4.8	820	2	G82168	trimethylamine-N-O	1213	67	4.8	459	1	DNHUN4	NADH2 dehydrogenas
1141	67.5	4.8	823	2	S44873	ZC21.2 protein - C	1214	67	4.8	461	2	H97568	manganese transpor
1142	67.5	4.8	823	2	B1282	probable integral	1215	67	4.8	462	2	T34365	hypothetical prote
1143	67.5	4.8	890	2	H69877	calcium-transporti	1216	67	4.8	468	2	AD0521	probable symporter
1144	67.5	4.8	900	2	D97351	sensor protein Kdp	1217	67	4.8	469	2	T35670	hypothetical prote
1145	67.5	4.8	936	2	B64567	cytochrome c bioge	1218	67	4.8	470	2	T26602	hypothetical prote
1146	67.5	4.8	952	2	T32836	hypothetical prote	1219	67	4.8	473	2	AG0612	probable transport
1147	67.5	4.8	1199	1	S76549	transcription-repa	1220	67	4.8	477	2	S71323	alpha-1A adrenergi
1148	67.5	4.8	1247	1	VHWV2	structural polypro	1221	67	4.8	485	2	C70488	cytochrome-c oxida
1149	67.5	4.8	1517	1	F65112	glutamate synthase	1222	67	4.8	491	2	G69251	proline permease (
1150	67.5	4.8	1517	2	F85985	glutamate synthase	1223	67	4.8	494	2	AC0133	probable permease
1151	67.5	4.8	1517	2	C91140	glutamate synthase	1224	67	4.8	511	2	H90439	hypothetical prote
1152	67.5	4.8	1704	2	T42749	ATP-binding cass	1225	67	4.8	516	2	T33269	hypothetical prote
1153	67.5	4.8	1767	2	S60124	transport protein	1226	67	4.8	517	2	AC2070	Na+/H+ antiporter
1154	67.5	4.8	1778	2	AF1116	internalin protein	1227	67	4.8	517	2	E82147	hypothetical prote
1155	67.5	4.8	2701	2	S17796	inositol-trisphosp	1228	67	4.8	522	2	F86215	protein T6D22.18 [
1156	67	4.8	90	2	E82861	conjugal transfer	1229	67	4.8	527	2	T49241	pectinesterase-lik
1157	67	4.8	109	2	C98018	crcB protein [mpo	1230	67	4.8	537	2	D70478	conserved hypochet
1158	67	4.8	168	2	A72286	conserved hypochet	1231	67	4.8	546	2	AE0571	probable membrane
1159	67	4.8	180	2	C86290	hypothetical prote	1232	67	4.8	557	2	T46520	probable transmemb
1160	67	4.8	187	2	A95143	membrane protein (1233	67	4.8	557	2	S58688	probable transport
1161	67	4.8	187	2	G98010	conserved hypochet	1234	67	4.8	557	2	G69096	hypothetical prote
1162	67	4.8	226	2	S57521	probable arsenical	1235	67	4.8	574	2	T41068	hypothetical prote
1163	67	4.8	232	1	G64591	conserved hypochet	1236	67	4.8	574	2	T34208	hypothetical prote
1164	67	4.8	259	2	S93132	cytochrome-c oxida	1237	67	4.8	584	2	B82810	ABC transporter ni
1165	67	4.8	260	2	A91138	hypothetical prote	1238	67	4.8	605	2	A36361	glucose transport
1166	67	4.8	260	2	D65110	hypothetical 27.9	1239	67	4.8	625	2	T33792	hypothetical prote
1167	67	4.8	261	2	D85983	hypothetical prote	1240	67	4.8	625	2	AD2251	two-component sens
1168	67	4.8	261	2	T11826	cytochrome-c oxida	1241	67	4.8	640	2	D90174	hypothetical prote
1169	67	4.8	265	2	T05668	pollen allergen ho	1242	67	4.8	644	2	S44478	NADH2 dehydrogenas
1170	67	4.8	268	2	C86944	probable cation-ef	1243	67	4.8	653	2	T19245	hypothetical prote
1171	67	4.8	278	2	A99349	bacitracin resista	1244	67	4.8	659	2	C65022	yfgg protein - Esc
1172	67	4.8	285	2	A84224	cytochrome c oxida	1245	67	4.8	698	2	T12586	NADH2 dehydrogenas
1173	67	4.8	287	2	B99936	hypothetical prote	1246	67	4.8	698	2	T12568	NADH2 dehydrogenas
1174	67	4.8	288	2	I78556	membrane glycoprot	1247	67	4.8	698	2	S76532	NADH2 dehydrogenas
1175	67	4.8	291	2	S48977	hypothetical prote	1248	67	4.8	699	2	T13778	NADH2 dehydrogenas
1176	67	4.8	293	2	D86065	glucose-1-phosphat	1249	67	4.8	707	2	G86894	hypothetical prote
1177	67	4.8	293	2	B91219	glucose-1-phosphat	1250	67	4.8	741	1	S34218	1,4-alpha-glucan b
1178	67	4.8	293	2	H65182	glucose-1-phosphat	1251	67	4.8	741	2	T13764	NADH2 dehydrogenas
1179	67	4.8	308	2	H64409	hypothetical prote	1252	67	4.8	878	2	A87385	tonB-dependent rec
1180	67	4.8	313	2	T24994	hypothetical prote	1253	67	4.8	918	2	A44257	interleukin-6 sign
1181	67	4.8	313	2	C95247	conserved hypochet	1254	67	4.8	970	2	F64230	spore germination
1182	67	4.8	313	2	H98111	conserved hypochet	1255	67	4.8	1001	2	T13807	potassium channel
1183	67	4.8	314	2	F81699	peptide ABC transp	1256	67	4.8	1218	2	S38182	probable transport
1184	67	4.8	323	2	AB0427	octaprenyl-dipho	1257	67	4.8	1440	2	JC6312	protein-tyrosine-p
1185	67	4.8	328	2	D72566	hypothetical prote	1258	67	4.8	1457	1	A48066	protein-tyrosine-p
1186	67	4.8	349	2	AD0990	probable membrane	1259	67	4.8	1489	2	S73015	polyketide synthas
1187	67	4.8	354	2	C92038	nitrogen regulatio	1260	67	4.8	1559	2	A12348	ferredoxin-glutama
1188	67	4.8	356	2	B84749	hypothetical prote	1261	67	4.8	1758	2	F88559	protein C4884.4b [
1189	67	4.8	364	2	T24418	hypothetical prote	1262	67	4.8	2183	2	S47307	genome polypeptid
1190	67	4.8	364	2	T45253	probable antiporte	1263	66.5	4.8	175	2	A95058	conserved domain p
1191	67	4.8	367	2	S23349	hypothetical prote	1264	66.5	4.8	175	2	B97927	hypothetical prote
1192	67	4.8	371	2	D97790	octaprenyl-dipho	1265	66.5	4.8	185	2	D81327	probable integral
1193	67	4.8	377	2	B71699	cell division prot	1266	66.5	4.8	205	2	A87460	DedA family protei
1194	67	4.8	388	2	B64459	Na+/H+-exchangin	1267	66.5	4.8	217	2	B69396	hypothetical prote
1195	67	4.8	394	2	AH0020	conserved integral	1268	66.5	4.8	245	2	F71887	hypothetical prote
1196	67	4.8	397	2	B70763	probable membrane	1269	66.5	4.8	256	2	G82804	phosphatidyltransf
1197	67	4.8	401	2	H82175	multidrug resistan	1270	66.5	4.8	258	2	A69830	hypothetical prote

1271	66.5	4.8	261	2	164249	hypothetical prote	1344	66.5	4.8	744	2	T13063	NADH2 dehydrogenas
1272	66.5	4.8	269	2	A86989	zinc ABC transport	1345	66.5	4.8	744	2	T13048	NADH2 dehydrogenas
1273	66.5	4.8	279	2	E69246	hypothetical prote	1346	66.5	4.8	746	2	T01536	hypothetical prote
1274	66.5	4.8	292	2	A70546	probable menA prot	1347	66.5	4.8	755	2	T20950	cellulose synthase
1275	66.5	4.8	292	2	F83823	hypothetical prote	1348	66.5	4.8	759	2	D70422	hypothetical prote
1276	66.5	4.8	293	2	T41928	hypothetical prote	1349	66.5	4.8	790	2	G90477	hypothetical prote
1277	66.5	4.8	295	2	AE0993	glycerol-3-phospha	1350	66.5	4.8	812	2	T16621	helicase - human h
1278	66.5	4.8	305	2	C70141	oligopeptide ABC t	1351	66.5	4.8	820	2	T41978	mannosyltransferas
1279	66.5	4.8	306	2	S55047	ABC-type transport	1352	66.5	4.8	860	2	C82750	glutamate receptor
1280	66.5	4.8	320	2	T23635	hypothetical prote	1353	66.5	4.8	919	2	T19810	olfactory channel -
1281	66.5	4.8	361	2	T37938	hypothetical prote	1354	66.5	4.8	919	2	I53474	protein B0212.5 [i
1282	66.5	4.8	366	2	G95376	conserved hypoteth	1355	66.5	4.8	937	2	T37241	hypothetical prote
1283	66.5	4.8	375	2	T05707	phosphate transpor	1356	66.5	4.8	957	2	D86651	hypothetical prote
1284	66.5	4.8	385	2	B87441	rod shape-determin	1357	66.5	4.8	999	2	T27628	conserved membrane
1285	66.5	4.8	389	2	AD1378	cell division prot	1358	66.5	4.8	1002	2	G97217	H+-exporting ATPas
1286	66.5	4.8	390	2	AD0260	conserved hypoteth	1359	66.5	4.8	1010	1	FX2P2P	hypothetical prote
1287	66.5	4.8	394	2	T13721	NADH2 dehydrogenas	1360	66.5	4.8	1049	2	T22762	B. subtilis YueB p
1288	66.5	4.8	402	2	T40193	hypothetical prote	1361	66.5	4.8	1068	2	AB1082	probable olfactory
1289	66.5	4.8	409	2	B85735	probable membrane	1362	66.5	4.8	1088	2	H84604	autolysin importe
1290	66.5	4.8	410	2	E75290	preprotein translo	1363	66.5	4.8	1248	2	C89874	ATP-binding cassel
1291	66.5	4.8	411	2	S73218	hypothetical prote	1364	66.5	4.8	1704	2	A59188	probable Atp-bind
1292	66.5	4.8	421	2	E90883	hypothetical prote	1365	66	4.7	1704	2	G71363	hypothetical prote
1293	66.5	4.8	422	2	H69839	multidrug resistan	1366	66	4.7	101	2	G69894	hypothetical prote
1294	66.5	4.8	428	2	G82918	hypothetical prote	1367	66	4.7	105	2	AH2209	probable olfactory
1295	66.5	4.8	438	2	H91112	hypothetical prote	1368	66	4.7	158	2	S58016	amis protein - Pse
1296	66.5	4.8	467	2	T16319	hypothetical prote	1369	66	4.7	171	2	S44146	hypothetical prote
1297	66.5	4.8	469	2	H70826	probable narX3 pro	1370	66	4.7	172	2	A83226	alpha-crystallin c
1304	66.5	4.8	471	2	F71543	probable dicarboxy	1371	66	4.7	195	1	CYH1AM	hypothetical prote
1305	66.5	4.8	472	2	E83497	probable amino aci	1372	66	4.7	196	2	AD2304	hypothetical prote
1306	66.5	4.8	474	2	S07754	NADH2 dehydrogenas	1373	66	4.7	203	2	T05519	hypothetical prote
1307	66.5	4.8	475	2	T46745	arginine/ornithine	1374	66	4.7	203	2	C85288	hypothetical prote
1308	66.5	4.8	478	2	D64895	probable membrane	1375	66	4.7	204	2	D69097	hypothetical prote
1309	66.5	4.8	480	2	D90038	PTS system, sucros	1376	66	4.7	211	2	E89863	hypothetical prote
1310	66.5	4.8	484	2	E75138	osmoregulated prol	1377	66	4.7	255	2	AH0577	molycoprotein-cont
1311	66.5	4.8	491	2	H84379	4-hydroxybutyrate	1378	66	4.7	256	2	JQ1106	tonoplast intrinsi
1312	66.5	4.8	492	2	T15603	hypothetical prote	1379	66	4.7	260	2	AG0904	probable ABC transp
1313	66.5	4.8	498	2	A10482	phosphate transpor	1380	66	4.7	265	2	H90254	sulfate ABC transp
1314	66.5	4.8	499	2	A65085	probable low-affin	1381	66	4.7	267	2	A87233	conserved membrane
1315	66.5	4.8	509	2	T11043	cytochrome-c oxida	1382	66	4.7	275	2	F83222	Nosy protein PA339
1316	66.5	4.8	513	2	T14864	probable monosacch	1383	66	4.7	276	2	B35252	hema concentration
1317	66.5	4.8	513	2	C81859	probable integral	1384	66	4.7	280	2	F75057	hypothetical prote
1318	66.5	4.8	519	2	E90548	conserved hypoteth	1385	66	4.7	285	2	S44085	plasma membrane in
1319	66.5	4.8	520	2	D90014	hypothetical prote	1386	66	4.7	285	2	D84789	hypothetical prote
1320	66.5	4.8	526	2	H85891	hydrogenase 4 memb	1387	66	4.7	285	2	D84789	hypothetical prote
1321	66.5	4.8	526	2	E65024	hydrogenase-4 comp	1388	66	4.7	296	2	G72760	NADH2 dehydrogenas
1322	66.5	4.8	530	2	T11884	cytochrome-c oxida	1389	66	4.7	298	2	T13684	conserved hypoteth
1323	66.5	4.8	553	2	T38541	probable vacuolar	1390	66	4.7	303	2	AB1772	hypothetical prote
1324	66.5	4.8	557	2	T49811	probable sodium/hy	1391	66	4.7	307	2	T16457	permease [imported
1325	66.5	4.8	569	2	T37706	probable sodium/hy	1392	66	4.7	311	2	AI2697	branched-chain ami
1326	66.5	4.8	573	2	T23102	hypothetical prote	1393	66	4.7	311	2	B97480	hypothetical prote
1327	66.5	4.8	574	2	G84578	probable potassium	1394	66	4.7	312	2	G69423	hypothetical prote
1328	66.5	4.8	648	2	C97961	DNA topoisomerase	1395	66	4.7	312	2	H90517	hypothetical prote
1329	66.5	4.8	648	2	F95093	DNA gyrase chain B	1396	66	4.7	318	2	AI1811	hypothetical prote
1330	66.5	4.8	649	2	AB2154	hypothetical prote	1397	66	4.7	320	2	T25308	NADH2 dehydrogenas
1331	66.5	4.8	659	2	S67175	probable membrane	1398	66	4.7	322	2	T13486	conserved hypoteth
1332	66.5	4.8	660	1	S54746	cytochrome c-type	1399	66	4.7	330	1	H69798	hypothetical prote
1333	66.5	4.8	664	2	B53610	ntpI protein - Ent	1400	66	4.7	335	2	T39425	hypothetical prote
1334	66.5	4.8	679	2	H95036	glycosyl hydrolase	1401	66	4.7	336	2	T31762	hypothetical prote
1335	66.5	4.8	699	2	T12173	NADH2 dehydrogenas	1402	66	4.7	344	2	AB3236	hypothetical prote
1336	66.5	4.8	703	2	H86588	thio,disulfide int	1403	66	4.7	354	2	S70595	NADH2 dehydrogenas
1337	66.5	4.8	703	2	H72034	thiol-disulfide in	1404	66	4.7	355	2	A64138	rfe protein - Haem
1338	66.5	4.8	714	2	G81503	thiol-disulfide in	1405	66	4.7	357	2	T03557	probable integral
1339	66.5	4.8	725	2	S52990	phenylalanine ammo	1406	66	4.7	357	2	F81916	N-acyl-L-amino aci
1340	66.5	4.8	732	2	AD0014	primosomal protein	1407	66	4.7	371	2	AD1201	hypothetical prote
1341	66.5	4.8	737	2	D97907	alpha-xylosidase (1408	66	4.7	377	2	H64387	hypothetical prote
1342	66.5	4.8	741	2	T12605	NADH2 dehydrogenas	1409	66	4.7	381	2	C71680	hypothetical prote
1343	66.5	4.8	741	2	T13361	NADH2 dehydrogenas	1410	66	4.7	383	2	E87680	neutral amino acid
							1411	66	4.7	395	2	A86527	neutral amino acid
							1412	66	4.7	395	2	E72095	MFS permease [impo
							1413	66	4.7	396	2	AH2859	probable transport
							1414	66	4.7	396	2	F97636	mg2+ transport pro
							1415	66	4.7	398	2	H75043	membrane protein y
							1416	66	4.7	404	2	S65991	

C;Genetics:
A;Gene: CESP:C33A11.2
A;Map position: X
A;Introns: 26/1; 117/3; 177/1; 208/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C33A11.2

Query Match 20.78; Score 288; DB 2; Length 271;
Best Local Similarity 30.98; Pred. No. 1e-17;
Matches 71; Conservative 43; Mismatches 104; Indels 12; Gaps 6;

QY 14 ALVITWTAATFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYIV 73
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Db 18 ALIFFVQSFFV--YTIADVLDVDPIFFYLLSSAADKRPQSCIFAIGANISSVLLALVVFV 75
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QY 74 RYKQVHALSP--ENVVIKLNKAGLVGILSCILGSLIVANFQKTLTPAAHVSGAVLTFGM 131
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 76 RYRLQGFIFAYDEANLQANWROKWFYGAALGLFFVANVQETAIIPVHMSSAVASFGG 135
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QY 132 GSLVMFVQTILSYOMQPKIHGKQVFWIRLLLVIM--CGVSALSM-LTCCSSVLHSGNFGT 187
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Db 136 FSIYIMIFQCYLTHRVTTITLTVFYIRVFTIPSVICFCCSFGFGIAASKIFKTY--P 193
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QY 188 DLEOKLHNPE--DKGYVLHMITTAEMSWSFSGFFGLTYIRDFQKISL 235
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 194 DLPTPRWSRIYQPGYELHQISALAEWGCAISQIFFIQSGFGPEFEDISL 243
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
RESULT 3
C88456
protein W03A5.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C88456
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: C88456
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <STO>
A;Cross-references: GB:chr_III; PIDN:AAAS0731.1; PID:9485161; GSPDB:GN00021; CESP:W03A5.
A;Note: weakly similar to gamma-glutamyl carboxylase
C;Genetics:
A;Gene: W03A5.2
A;Map position: 3

Query Match 8.68; Score 120; DB 2; Length 547;
Best Local Similarity 21.88; Pred. No. 0.01;
Matches 48; Conservative 46; Mismatches 100; Indels 26; Gaps 9;

QY 51 PEKCLFGAMLNIAAVLCIATYIVRYKQVHALSPEN---VIIKLNKAGLVGILSCILGLS 107
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 14 PAKNAYIMTNHILLISVMWLYKRELKSPFRANISIFIKGSRVNLFIGLAALTSYQ 73
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
QY 108 IVANFQKTLTPAAHVSGAVLTFGMGSLYMFVQTILSYOMQPKIHGKQVFWIRLLLVWCG 167
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 74 LAVNFPATKINHVALIGNKLLANLYWHPFLSPKIR---DCGNPRWILFLIRI--- 127
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
QY 168 VSALSMLTCCSSVLHSGNFGTDLQKLHNPE-DKGYVLHMITTAEMSWSFSGFFELTY 226
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 128 --SLAFVVS-----LGAAMIQ-ANWVPDPSKOYL--AIDAIYWCYCFACVFLTLD 175
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
QY 227 IRDFQKISLR-VEANLHGLTYLDT---APCPINNERTLL 262
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 176 AYEFRFMFKPKLIIRGCTGYNERVESCDSDEDNLT 215
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
RESULT 4
E69312
nitrate reductase gamma subunit homolog - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69312
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69312
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-332 <KLE>
A;Cross-references: UNIPROT:O29749; GB:AE001069; GB:AE000782; MID:g2689392; PIDN:AA89073

Query Match 7.48; Score 103; DB 2; Length 332;
Best Local Similarity 17.08; Pred. No. 0.18;
Matches 45; Conservative 47; Mismatches 112; Indels 60; Gaps 8;

QY 2 WNFQQLSFL-----PSALVITWTSAAFIPIFYITAVTLHH---I 36
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 65 WNETAGRMILLEIFFFRSLKNTYYLDYRSQKDARWLFGILFHYSLLLVLRHSRFFL 124
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
QY 37 DPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYIVRYKQVHALSPENVIKLNKAGL 96
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 125 DVPSEFVETLSEIEAFKGVFIPIVYMSGLAIVAAFLMLRRIFLSRERTLSLPSPHFAL 184
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
QY 97 VLGILSCILGSLIVANFQKTLTPAA-HVSGAVLTFGMGSLYMFVQTILSYOMQPKIHGKQV 155
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 185 ILLLAITISGNVRYFVKADLFAVKELLSLMTFNIGHAVEVANTI-----EPI 233
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
QY 156 FWRLLLVTCGVSALSMLTCCSSVLHSG-----NFGTDLEQKUH---WNPEDKGYVL 204
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 234 FYVHFALASF---LLAYFPFKLMHAGGVFFSPTRNMPDNRRHRVHPWDPADVPFLA 289
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
QY 205 HMITTAA-----EWSMSFSFPF 220
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 290 KGITVAGRVYKSKLDWDYIYSY 313
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
RESULT 5
AI0561
integral membrane protein Aefa [imported] - Salmonella enterica subsp. enterica serovar
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0561
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
., S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0561
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1120 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD04963.1; PID:gl6501750; GSPDB:GN00176
C;Genetics:
A;Gene: STY0522

Query Match 7.18; Score 98.5; DB 2; Length 1120;
Best Local Similarity 19.58; Pred. No. 1.6;
Matches 58; Conservative 46; Mismatches 101; Indels 93; Gaps 11;

QY 1 MNWFQQLSFLPSALVITWTSAAFIPIFYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 805 MFW-----AIWSDLTITVSYLSDISITLWHYNG-----SEGAADVKSVTWGSLL 847
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
QY 61 -----NIAAVLCIATYIVRYKQVHALSPENVIKLNKAGLVGLS- 102
|||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
nitrate reductase gamma subunit homolog - Archaeoglobus fulgidus

Db 848 FAIAAMVAMALIRNLPGCLLEVLVSLRLNMRQGSAYAITTLNVLIIAVGAMTVFGSLGV 907
Qy 103 -----CIGLSIVANFQKTTLEAAHVSGAVLTF-----GMSLYMP 137
Db 908 SWDKQLWLAALASVGLGFLQEIFCNFVSGIILIFERPVRIGDVTVTIGTSGTVSKIR 967
Qy 138 VQTILSYQMOPKIHGQVFWIRLLLVICWGVSAISMLTSCSVLHSG-NFGTDLBOKLHWN 196
Db 968 ATTITDFDRKEVILPNKAF-VTERLINW-----SLSDTTTRLVIRLGVAYGSDLEK----- 1017
Qy 197 PEDKGYVLHMITTAA-----EWSMSPSFFGF-----FUYIRDFQKISLRVE 238
Db 1018 -----VKRVLLQAAMEHPKVMHDPKPAVPTTFEGASTDLHELRLYVRELDRDRSHSTD 1069
RESULT 6
E72523
carbon starvation protein A homolog APE2162 [similarity] - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E72523
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72523
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-604 <KAW>
C:Cross-references: UNIPROT:Q9Y9X7; DDBJ:AP000063; NID:G5105654; PIDN:BAAB1173.1; PID:G5
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2162
C:Superfamily: carbon starvation protein
Query Match 7.0%; Score 97; DB 2; Length 604;
Best Local Similarity 23.9%; Pred. No. 1.1;
Matches 69; Conservative 39; Mismatches 101; Indels 80; Gaps 16;
Qy 4 FQOGLSFLPSAL--VIVTSAAFIFSYYTAVTLHHIDPALPYISDTGTVAPEKCLFGAMLN 61
Db 183 YRMGLGMPSTVITVVLVIAAFVSYNHHGIVIGTFDPSLP-PGEGGWVAYHRWVI--ILG 239
Qy 62 IAAVLCTIATYVRKQVHALSPENVIKLNKAGLIVGLISCLGLSIVANFQKTTLFAAH 121
Db 240 LYALLA-ASLPVWY-----LLQPRD-----YLNAYILWTG-----LGLAAIA---AII LGTQS 283
Qy 122 VSGAVLTFGMSLYMFVQTILSYQMOPKIHGQVFWIRLLLVICWGVSAISMLTSCSVLH 181
Db 284 LKGPAYT-----SFGPNIIAGQPTP-----FWPAIPIIIACG-----SLSGFHSIVA 325
Qy 182 SGNFGTDLQKLNH-----WN-PE--DKGYV-LHMITTA 210
Db 326 SGTTSKQLASELDALFVYGAMLEGALSGLAVIIPISFANWAFELIKQGVNIENMLDLA 385
Qy 211 A-----EWSMSPSFFGFYTYIRDFQKISLRVEANLHGLTLYDT 249
Db 386 AVPRYAVGYGYTLAKTEPMFGVGDGTGYSFFTLFASLMSLYVLTILD 434
RESULT 7
S43882
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - garden lettuce mitochondrion
C:Species: mitochondrion Lactuca sativa (garden lettuce)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S43882
R;Geiss, K.T.; Abbas, G.M.; Makaroff, C.A.
Mol. Gen. Genet. 243, 97-105, 1994
A>Title: Intron loss from the NADH dehydrogenase subunit 4 gene of lettuce mitochondrion
A:Reference number: S43882; MUID:94247363; PMID:8190077
A:Accession: S43882

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-495 <GEI>
A:Cross-references: UNIPROT:Q37544
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 6.9%; Score 96; DB 2; Length 495;
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 55; Conservative 34; Mismatches 83; Indels 52; Gaps 12;
Qy 8 LSLPSALVITWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI--- 62
Db 277 LCFTT--FIYTLISAIIYTSLLTLRQID--LKKIIAYSSVAHMLNLTTCMFSLNIQGI 331
Qy 63 -----RAVLCIATYVRYKQ-----VHALSPENVIKLNKAGLVL 98
Db 332 GGSILLMLSHGLVSSALFLCVGLYVRHTRLVRYGGLVSTPNFSTIFFFTFLANMSL 391
Qy 99 -GILSCILG--LSIVANFQKTTLFAAHVSGAVLTFGMSLYMFVQTILSYQMOP----- 148
Db 392 PGTSSSIFGEFLIIVGAFQFNSLVATLAALGMILGAAYSLWLY-NRVVSGNLKPDPLHKFS 450
Qy 149 KIHGQVFWIRLLL-VIVCGVSALSMLTC-----SSVLHSGNP 185
Db 451 DLNGTEVFIFPIPELVGVVMGVYKVPFPCDMHTSVSNLVQHGKF 494
RESULT 8
S16447
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - wheat mitochondrion
N;Alternate names: mitochondrial complex I subunit IV
C:Species: mitochondrion Triticum aestivum (common wheat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S16447; S16448; S06835
R;Lamattina, L.; Grienemberger, J.M.
Nucleic Acids Res. 19, 3275-3282, 1991
A>Title: RNA editing of the transcript coding for subunit 4 of NADH dehydrogenase in whe
A:Reference number: S16447; MUID:91288205; PMID:1712098
A:Accession: S16447
A:Molecule type: mRNA
A:Residues: 1-495 <LAM>
A:Cross-references: UNIPROT:P27572; EMBL:X57163
A>Note: the authors translated the codon CGT for residue 418 as Ala
A:Accession: S16448
A:Molecule type: DNA
A:Residues: 1-14, P, 16-24, TP, 27-35, P, 37-51, PP, 54, PR, 57-65, S, 67-105, S, 107-120
'H', 474-477, P, 479-495 <LAF>
A:Cross-references: EMBL:X57164; NID:G21823; PIDN:CAA40453.1; PID:G21824
A>Note: the authors translated the codon CGT for residue 418 as Ala
A>Note: 15-P, 25-Thr, 26-Pro, 36-Pro, 52-Pro, 53-Pro, 55-Pro, 56-Arg, 66-Ser, 106-Ser, 1
re due to RNA editing
R;Lamattina, L.; Weil, J.H.; Grienemberger, J.M.
FEBS Lett. 258, 79-83, 1989
A>Title: RNA editing at a splicing site of NADH dehydrogenase subunit IV gene transcript
A:Reference number: S06835; MUID:90076495; PMID:2687023
A:Accession: S06835
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 295-346 <LAW>
C:Genetics:
A:Gene: nad4
A:Genome: mitochondrion
A:Introns: 154/2; 326/1; 467/1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 6.8%; Score 94; DB 1; Length 495;
Best Local Similarity 24.1%; Pred. No. 1.7;
Matches 54; Conservative 34; Mismatches 84; Indels 52; Gaps 11;
Qy 8 LSLPSALVITWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI--- 62

Db 277 LCFTP---FIYLSAIIYVTSLLTLRQID--LKKIIAYSSVAHMLVTIGMFSNLQIGI 331

Qy 63 -----AAVLCIATIIYVRYKO-----VHALSPENVIKLNKAGLV 98

Db 332 GGSILLMLSHGLVSSALFLCVGLYDRHKRLVRYVYGGVSTWPNFSTIFFFTFLANMSL 391

Qy 99 -GILSLCIG--LSIVANFQKTTLFAAHVSGAVLTFGMSLYMFVQTTLSYQMQP----- 148

Db 392 PGTSSFFIGEFILIVGAFQNSLVATLRALGMILGAAYSLMWLY-NRVVSGNLKPDFLYKPS 450

Qy 149 KIRGKQVFWIR--LLLVIWCGVSALSMLTC-----SSVLHSGNF 185

Db 451 DLNGREVFIFLPFLGVVWVGVPKVFDCMHTSVSNLVQHGF 494

RESULT 9

D96506

hypothetical protein T12C22.2 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: D96506

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D96506

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <STO>

A:Cross-references: UNIPROT:Q9LPP6; GB:AE005173; NID:g8655985; PIDN:AAF78258.1; GSPDB:GN

C:Genetics:

A:Gene: T12C22.2

A:Map position: 1

C:Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70

Query Match 6.7%; Score 93.5; DB 2; Length 379;

Best Local Similarity 21.8%; Pred. No. 1.4;

Matches 47; Conservative 53; Mismatches 95; Indels 21; Gaps 9;

Qy 10 FLPSALVWITSAAFIPIFYITAVTLHHIDPALPYISDTGTVAPEKCLFG-AMLNIAA---- 64

Db 90 YIP--LLLLPSSASVESSESSCSLYI--VLIYVLLGVIIAGDNMLYSVGLLYLSASTYS 145

Qy 65 VLCIATIIYRYKQVHALSPENVIKLNKAGLVGLISLCGLSIVANFQKTTLFAAHVSG 124

Db 146 LICATQLAFNAVFSYFNAQKFTALILNSVLLSFSAAALIALDADATPSGVSRSKYVG 205

Qy 125 AVLTFGMSLYMFVQTTLSYQMQPKHGKQVFWIRLLLVWCGVSALSMLTCSSVLHSGN 184

Db 206 FVCTLAASALYSLLLSLMQSPFE-KILKRTFTSVLEMQIYTSIVA----TCVSVI--GL 258

Qy 185 FGTDLEOKLHNPE--DKG---YVLHMITTAESWM 215

Db 259 FASGEWRTLHGEYGHKGQASVVLTLVWTAVTQV 294

RESULT 10

F71651

putrescine-ornithine antiporter (potE) RP483 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C:Accession: F71651

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: F71651

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-429 <AND>

A:Cross-references: UNIPROT:Q9ZD63; GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA1493

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: potE; RP483

C:Superfamily: L-lysine transport protein

Query Match 6.7%; Score 93.5; DB 2; Length 429;

Best Local Similarity 24.1%; Pred. No. 1.6;

Matches 48; Conservative 37; Mismatches 79; Indels 35; Gaps 10;

Qy 11 LPSALVWITSAAFIPIFYITAVTLHHIDPA-----LPYISDTGTVAPEKCLFGAMLN-- 61

Db 217 IPRAIIIGTCVAFIYIINSIGIIGLIPASELINSKAPY-ADAATL-----LFGGTWSKV 270

Qy 62 ---IAAVLCIATI---YVRYKQVHALSPENVIKLN-----NKAGLVGLISLCGLSIV 109

Db 271 ITVIASVICIGTILNAWLTSGQIALGLAEDGLLPKFFAKKNSNNAPTYGIIISCLGITEL 330

Qy 110 ANFQKTTTLFAAHVSGAVLTFGMSLYMFVQTTLSYQMQPKI-HGKQVFWIRLLLVWCGV 168

Db 331 LLFTSNNNFAKQIT-QIIDFSV-IAFLFVYLICSLAFLKVIFFSKENFYSYVLF-----V 383

Qy 169 SALSMLTCSSVLHSGNFGT 187

Db 384 AIISIIFTWVIYKTPPET 402

RESULT 11

F90693

mechanosensitive channel protein [imported] - Escherichia coli (strain O157:H7, substrain

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: F90693

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F90693

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1120 <HAY>

A:Cross-references: UNIPROT:Q8XD54; GB:BA000007; PIDN:BA33941.1; PID:g13359975; GSPDB:G

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs0518

Query Match 6.7%; Score 93; DB 2; Length 1120;

Best Local Similarity 19.6%; Pred. No. 5;

Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;

Qy 1 MWFFQGLSFLPSALVWITSAAFIPIFYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Db 805 MPW-----AIWSDLITVFSYLSITLWHYNG-----TEGAADVKNVTWGSLL 847

Qy 61 -----NIAAVLCIATIIYRYKQVHALSPENVIKLNKAGLVGLIS- 102

Db 848 FAIIASMWAWALIRNLPGLEVLVLSRLNMRQASVAITILNYIIIAVGAMTVFGSLGV 907

Qy 103 -----CLGLSIVANFQKTTLFAAHVSGAVLTF-----GMGSLYMF 137

Db 908 SMDKLQWLAALASVGLGQLQIFGNFVSGILFIRPVRIGTIVTIGSFGTSVKIRIR 967

Qy 138 VOTILSYQMQPKIHGKQVFWIRLLLVWCGVSALSMLTCSSVLHSG-NFGTDLEQ 191

Db 968 ATTITDFDKREVIIPNKA-FVTERLINW----SLDTTTLVRLGVAYGSDLEK 1017

RESULT 12

[illegible]

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OM protein - protein search, using sw model

Run on: August 26, 2005, 17:15:16 ; Search time 174 Seconds
(without alignments)
782.834 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MNFQGLSFLPSALVWTS.....YDTAPCPINNERTLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1392	100.0	266	2	Q6UX65
2	1245	89.4	267	2	Q9CR48
3	1235	88.7	267	2	Q9D520
4	1078	77.4	208	2	Q86VD3
5	805.5	57.9	180	2	Q9D835
6	764.5	54.9	272	2	Q6IQ10
7	725	52.1	136	2	Q8NB04
8	492.5	35.4	238	2	Q8N682
9	479.5	34.4	238	2	Q9DC58
10	471.5	33.9	287	2	Q6NR36
11	439.5	31.6	238	2	Q8QG82
12	388.5	27.9	282	2	Q7QE61
13	361.5	26.0	246	2	Q77262
14	318.5	22.9	252	2	Q86F93
15	288	20.7	271	2	Q93319
16	262	18.8	238	2	Q8R218
17	251.5	18.1	181	2	Q6XHP5
18	251	18.0	132	2	Q9NUN1
19	240	17.2	132	2	Q78J26
20	203	14.6	249	2	Q8C853
21	201.5	14.5	271	2	Q8GPI4
22	191.5	13.8	257	2	Q6IQJ3
23	185.5	13.3	219	2	Q6P6P1
24	183.5	13.2	294	2	Q7SXX4
25	172.5	12.4	243	2	Q86IK0
26	161.5	11.6	123	2	Q8C9I9
27	160.5	11.5	271	2	Q86TG1
28	157.5	11.3	271	2	Q9Q2S9
29	151.5	10.9	271	2	Q91WN2
30	150.5	10.8	243	2	Q86K17
31	120	8.6	224	2	Q23135

32	112.5	8.1	252	2	Q9U3J7	Q9U3J7 caenorhabdi
33	106.5	7.7	140	2	Q8K117	Q8K117 mus musculu
34	103	7.4	299	2	Q6CDS5	Q6CDS5 yarrowia li
35	103	7.4	332	1	HMEC_ARCFU	O29749 archaeoglob
36	101.5	7.3	255	2	Q9VPT7	Q9VPT7 drosophila
37	101.5	7.3	332	2	Q6S0W2	Q6S0W2 oryza sativ
38	101	7.3	218	2	Q8N2R6	Q8N2R6 homo sapien
39	101	7.3	293	2	Q6SRP9	Q6SRP9 manheimia
40	101	7.3	495	1	NU4M_ARATH	P93313 arabidopsis
41	101	7.3	539	2	Q8EJE2	Q8EJE2 shewanella
42	98.5	7.1	456	2	Q6D428	Q6D428 erwinia car
43	98.5	7.1	1120	2	Q8Z8T6	Q8Z8T6 salmonella
44	98.5	7.1	1120	2	Q8ZRA5	Q8ZRA5 salmonella
45	98	7.0	495	2	Q8M8A9	Q8M8A9 beta vulgar
46	98	7.0	495	2	Q6YSN0	Q6YSN0 brassica na
47	97.5	7.0	664	2	Q966D8	Q966D8 caenorhabdi
48	97.5	7.0	746	2	Q9NSQ9	Q9NSQ9 caenorhabdi
49	97	7.0	390	2	Q8XQMO	Q8XQMO ralbstonia s
50	97	7.0	604	2	Q9Y9X7	Q9Y9X7 aeropyrum p
51	96	6.9	395	2	Q8EPB8	Q8EPB8 shewanella
52	96	6.9	495	2	Q37544	Q37544 lactuca sat
53	96	6.9	615	2	Q7S1C6	Q7S1C6 neurospora
54	95.5	6.9	251	2	Q9ZFP3	Q9ZFP3 enterococcu
55	95.5	6.9	309	2	Q6NRD6	Q6NRD6 xenopus lae
56	95.5	6.9	486	2	Q8QF5	Q8QF5 corynebacte
57	95	6.8	702	2	Q9SC10	Q9SC10 tetracera a
58	94.5	6.8	469	2	Q7UF66	Q7UF66 rhodopirell
59	94.5	6.8	724	2	Q6FUL0	Q6FUL0 candida gla
60	94	6.8	283	2	Q88NV8	Q88NV8 pseudomonas
61	94	6.8	495	1	NU4M_WHEAT	P27572 triticum ae
62	94	6.8	1120	2	Q8FX90	Q8FX90 escherichia
63	93.5	6.7	379	2	Q9LFP6	Q9LFP6 arabidopsis
64	93.5	6.7	429	2	Q9ZD63	Q9ZD63 rickettsia
65	93	6.7	1120	1	KEPA_ECOLI	P77338 escherichia
66	93	6.7	1120	2	Q8XD54	Q8XD54 escherichia
67	93	6.7	1120	2	Q83SE8	Q83SE8 shigella fl
68	93	6.7	1264	2	Q6BT03	Q6BT03 debaryomyce
69	92.5	6.6	251	2	Q970A1	Q970A1 sulfolobus
70	92.5	6.6	473	2	Q8Z506	Q8Z506 salmonella
71	92.5	6.6	473	2	Q8ZNC5	Q8ZNC5 salmonella
72	92.5	6.6	479	2	Q6SGM5	Q6SGM5 uncultured
73	92.5	6.6	977	2	Q6CX54	Q6CX54 kluyveromyc
74	92	6.6	434	2	Q7VN68	Q7VN68 haemophilus
75	91.5	6.6	387	2	Q22188	Q22188 caenorhabdi
76	91.5	6.6	430	2	Q8I0L4	Q8I0L4 caenorhabdi
77	91.5	6.6	444	2	Q67EN8	Q67EN8 callinectes
78	91.5	6.6	495	2	Q9MF62	Q9MF62 beta vulgar
79	91.5	6.6	530	2	Q88W48	Q88W48 lactobacill
80	91.5	6.6	712	1	POTI_ARATH	O22397 arabidopsis
81	91.5	6.6	732	2	Q9TJY8	Q9TJY8 condaminea
82	91.5	6.6	1085	2	Q7VQP9	Q7VQP9 candidatus
83	91	6.5	257	2	Q6H1W4	Q6H1W4 bacillus th
84	91	6.5	372	2	Q8NXX5	Q8NXX5 staphylococ
85	91	6.5	552	2	Q7WNJ3	Q7WNJ3 bordetella
86	90.5	6.5	311	2	Q6CLU8	Q6CLU8 kluyveromyc
87	90.5	6.5	529	2	Q7QUJ9	Q7QUJ9 anophelies g
88	90.5	6.5	614	2	Q9LNF0	Q9LNF0 arabidopsis
89	90.5	6.5	1505	2	Q73JH5	Q73JH5 treponema d
90	90	6.5	283	2	Q8NUB1	Q8NUB1 corynebacte
91	90	6.5	396	2	Q8PFS3	Q8PFS3 escherichia
92	90	6.5	400	2	Q9KN80	Q9KN80 vibrio chol
93	90	6.5	492	1	NU4M_CHOCR	P48915 chondrus cr
94	90	6.5	528	1	YCD8_YEAST	P25568 saccharomyc
95	90	6.5	554	2	Q8GJF7	Q8GJF7 bdellovibri
96	90	6.5	557	2	Q877D2	Q877D2 pyrobaculum
97	90	6.5	739	2	Q6MKW0	Q6MKW0 bdellovibri
98	89.5	6.4	270	2	Q86CV4	Q86CV4 pseudomonas
99	89.5	6.4	437	2	Q9CL14	Q9CL14 pasteurella
100	89.5	6.4	440	1	DCUB_HAEIN	P44855 haemophilus
101	89.5	6.4	440	2	Q65QD7	Q65QD7 manheimia
102	89.5	6.4	443	2	Q929T2	Q929T2 listeria in
103	89.5	6.4	485	2	Q88T41	Q88T41 lactobacill
104	89.5	6.4	495	2	O59121	O59121 pyrococcus

105	89.5	6.4	579	2	Q8DZT0	Q8dzt0 streptococc	178	86	6.2	233	2	Q662P5	Q662p5 borrelia ga
106	89.5	6.4	579	2	Q8ESH7	Q8esh7 streptococc	179	86	6.2	234	2	Q8B3W1	Q8b3w1 mus musculus
107	89.5	6.4	599	2	Q220B9	Q220b9 caenorhabdi	180	86	6.2	237	2	Q6GAU7	Q6gau7 staphylococ
108	89.5	6.4	963	2	Q7R2T8	Q7r2t8 giardia lam	181	86	6.2	372	2	Q99VB1	Q99vb1 staphylococ
109	89	6.4	267	2	Q8BV59	Q8bv59 mus musculu	182	86	6.2	373	2	Q7A6G2	Q7a6g2 staphylococ
110	89	6.4	290	2	Q72YR6	Q72yr6 bacillus ce	183	86	6.2	389	2	Q9V0C0	Q9v0c0 pyrococcus
111	89	6.4	290	2	Q812M6	Q812m6 bacillus ce	184	86	6.2	396	1	BCR_ECOLI	P28246 escherichia
112	89	6.4	428	2	Q66FX2	Q66fx2 yersinia ps	185	86	6.2	444	2	Q7Y8W4	P28246 escherichia
113	89	6.4	428	2	Q8ZJ45	Q8zj45 yersinia ps	186	86	6.2	509	2	Q7R5J8	P28246 escherichia
114	89	6.4	442	2	Q7MP35	Q7mp35 vibrio vuln	187	86	6.2	667	2	Q8W9Q3	Q8w9q3 mesostigma
115	89	6.4	637	2	Q9H8H9	Q9h8h9 homo sapien	188	86	6.2	701	2	Q8HTM4	Q8htm4 achlys tripp
116	89	6.4	659	2	Q7VUY3	Q7vuy3 bordetella	189	86	6.2	703	2	Q9LMM3	Q9lmm3 arabidopsis
117	89	6.4	660	2	Q7WBD6	Q7wbd6 bordetella	190	86	6.2	725	2	P92949	P92949 arabidopsis
118	89	6.4	757	2	Q9UFA2	Q9ufa2 homo sapien	191	86	6.2	841	2	Q93QY7	Q93qy7 staphylococ
119	89	6.4	917	2	Q96F81	Q96f81 homo sapien	192	86	6.2	841	2	Q7VGA9	Q7vga9 helicobacte
120	89	6.4	917	2	Q9H698	Q9h698 homo sapien	193	86	6.2	954	2	Q8TEH2	Q8teh2 dictyostell
121	88.5	6.4	361	2	Q83F26	Q83f26 coxiella bu	194	85.5	6.1	1308	2	Q8TEH2	Q8teh2 dictyostell
122	88.5	6.4	430	2	Q9V210	Q9v210 pyrococcus	195	85.5	6.1	219	2	Q9CY24	Q9cy24 mus musculu
123	88.5	6.4	680	2	Q9SBV7	Q9sbv7 vahlia cape	196	85.5	6.1	219	2	Q9D8L7	Q9d8l7 mus musculu
124	88.5	6.4	691	2	Q8M8V0	Q8m8v0 vahlia cape	197	85.5	6.1	250	2	Q6CID8	Q6cid8 kluveromyc
125	88.5	6.4	732	2	Q9TJ0P3	Q9tj0p3 simira viri	198	85.5	6.1	261	2	Q9CP79	Q9cp79 pasteurella
126	88.5	6.4	732	2	Q9TJ52	Q9tj52 pentagonia	199	85.5	6.1	295	2	Q9K0I7	Q9k0i7 neisseria m
127	88.5	6.4	808	2	Q21453	Q21453 caenorhabdi	200	85.5	6.1	296	2	Q669X3	Q669x3 yersinia ps
128	88.5	6.4	833	2	Q7USM4	Q7usm4 rhodopirell	201	85.5	6.1	296	2	Q8ZF11	Q8zff1 yersinia ps
129	88	6.3	290	2	Q632P0	Q632p0 bacillus ce	202	85.5	6.1	311	1	PAQ3_HUMAN	Q669x3 yersinia ps
130	88	6.3	290	2	Q81KE4	Q81ke4 bacillus an	203	85.5	6.1	311	1	Q88TD9	Q88td9 lactobacill
131	88	6.3	290	2	Q6HC79	Q6hc79 bacillus th	204	85.5	6.1	329	2	Q96K55	Q96k55 homo sapien
132	88	6.3	372	2	Q8A1P0	Q8a1p0 bacteroides	205	85.5	6.1	355	2	Q8TNX8	Q8tnx8 methanosarc
133	88	6.3	413	2	Q8R792	Q8r792 thermoaer	206	85.5	6.1	399	2	Q7SPY5	Q7spy5 cavia porce
134	88	6.3	500	2	Q9TCC1	Q9tcc1 nephroselmi	207	85.5	6.1	401	2	Q89KV1	Q89kv1 bradyrhizob
135	88	6.3	546	2	Q8PXP0	Q8pxp0 methanosarc	208	85.5	6.1	458	2	Q8WUB5	Q8wub5 homo sapien
136	88	6.3	622	2	Q7S317	Q7s317 neurospora	209	85.5	6.1	498	2	Q21287	Q21287 reclinomona
137	88	6.3	660	2	Q7WMV6	Q7wmv6 bordetella	210	85.5	6.1	526	2	Q90X46	Q90x46 brachydanio
138	88	6.3	661	2	Q74F70	Q74f70 geobacter s	211	85.5	6.1	528	2	Q6A2J4	Q6a2j4 brandisia h
139	88	6.3	732	2	Q9TJ0P1	Q9tj0p1 warszewicz	212	85.5	6.1	545	1	Q96JZ5	Q96jz5 homo sapien
140	88	6.3	787	2	Q6SHL0	Q6shl0 uncultured	213	85.5	6.1	587	1	T9S3_MOUSE	Q96jz5 homo sapien
141	88	6.3	929	2	Q9LGC6	Q9lgc6 oryza sativ	214	85.5	6.1	589	1	T9S3_HUMAN	Q96jz5 homo sapien
142	88	6.3	1165	1	CYA6_CANFA	P30804 canis fami	215	85.5	6.1	589	1	T9S3_HUMAN	Q96jz5 homo sapien
143	87.5	6.3	215	2	Q9DZW6	Q9dzw6 mus musculu	216	85.5	6.1	696	2	Q9TIW8	Q9tiw8 phacelia ro
144	87.5	6.3	233	1	Y117_BORBU	O51144 borrelia bu	217	85.5	6.1	703	2	Q9TILAS	Q9ti1as jasinum me
145	87.5	6.3	365	2	Q6KH7	Q6khr7 mycoplasma	218	85.5	6.1	851	2	Q6FU89	Q6fu89 candida gla
146	87.5	6.3	429	2	Q68WP9	Q68wp9 rickettsia	219	85.5	6.1	999	2	Q93JY2	Q93jy2 erwina chr
147	87.5	6.3	429	2	Q9KR3	Q9krp3 vibrio chol	220	85	6.1	304	2	Q96U46	Q96u46 neurospora
148	87.5	6.3	453	1	TDE2_MOUSE	Q9qzi8 mus musculu	221	85	6.1	307	2	Q6F7C6	Q6f7c6 acinetobact
149	87.5	6.3	453	2	Q642W5	Q642w5 clymenella	222	85	6.1	333	2	Q6XCC9	Q6xc9 cyprinus ca
150	87.5	6.3	453	2	Q7TNK0	Q7tnk0 rattus norv	223	85	6.1	338	1	PSG1_MYCTU	P95303 mycobacteri
151	87.5	6.3	456	2	Q6BQ78	Q6bq78 debaryomyce	224	85	6.1	361	2	Q82V86	Q82v86 nitrosomona
152	87.5	6.3	482	1	YF1G_BACSU	P54723 bacillus su	225	85	6.1	369	2	Q9N2T7	Q9n2t7 caenorhabdi
153	87.5	6.3	530	2	Q8EM57	Q8emr7 oceanobacil	226	85	6.1	419	2	Q8NRU3	Q8nr3 corynebacte
154	87.5	6.3	544	2	Q18051	O18061 caenorhabdi	227	85	6.1	427	2	Q7PKH1	Q7pkh1 anopheles g
155	87.5	6.3	547	2	Q824X5	Q824x5 chlamydophi	228	85	6.1	443	2	Q9CEP2	Q9cep2 lactococcus
156	87.5	6.3	671	2	Q73WX6	Q73wx6 mycobacteri	229	85	6.1	462	2	Q96YE7	Q96ye7 sulfolobus
157	87.5	6.3	732	2	Q9TJ02	Q9tj02 rustia sple	230	85	6.1	497	2	Q6BY36	Q6by36 debaryomyce
158	87.5	6.3	1687	2	Q6Q117	Q6q117 rattus norv	231	85	6.1	498	2	Q9QXP0	Q9qxp0 mus musculu
159	87	6.2	261	2	Q7VLV2	Q7vlv2 haemophilus	232	85	6.1	522	2	Q9B8X9	Q9b8x9 fasciola he
160	87	6.2	271	2	Q6FF11	Q6ff11 acinetobact	233	85	6.1	524	2	Q8U4T9	Q8u4t9 halobacteri
161	87	6.2	396	2	Q8XSA2	Q8xsa2 escherichia	234	85	6.1	543	2	Q83GL8	Q83gl8 tropheryma
162	87	6.2	410	2	Q62B58	Q62b58 burkholderi	235	85	6.1	543	2	Q83HB2	Q83hb2 tropheryma
163	87	6.2	410	2	Q63LL0	Q63ll0 burkholderi	236	85	6.1	558	2	Q6XJ14	Q6xj14 sideroxylion
164	87	6.2	435	1	EXOQ_RHIME	Q92729 rhizobium m	237	85	6.1	658	2	Q6XJ14	Q6xj14 sideroxylion
165	87	6.2	613	2	Q9I4D1	Q9i4d1 pseudomonas	238	85	6.1	845	2	Q80Z08	Q80z08 mus musculu
166	87	6.2	928	2	Q9LEC9	Q9lec9 solanum tub	239	84.5	6.1	1166	1	CYA6_RAT	Q03343 rattus norv
167	86.5	6.2	301	2	Q970F4	Q970f4 sulfolobus	240	84.5	6.1	205	2	Q8BL29	Q8bl29 mus musculu
168	86.5	6.2	368	2	Q839R1	Q839r1 enterococcu	241	84.5	6.1	269	2	Q837L9	Q837l9 enterococcu
169	86.5	6.2	400	1	YCEI_BACSU	Q34691 bacillus su	242	84.5	6.1	283	2	Q6SD18	Q6sd18 bacillus li
170	86.5	6.2	440	2	Q9BK78	Q9bkt8 caenorhabdi	243	84.5	6.1	323	2	Q7MYX3	Q7myx3 photorhabdu
171	86.5	6.2	547	2	Q6N8M3	Q6n8m3 rhodopseudo	244	84.5	6.1	394	2	Q7Q0F3	Q7q0f3 anopheles g
172	86.5	6.2	557	2	Q8ZXC1	Q8zxc1 probaculum	245	84.5	6.1	395	2	Q6ND83	Q6nd83 rhodopseudo
173	86.5	6.2	583	2	Q8Y9B6	Q8y9b6 listeria mo	246	84.5	6.1	405	2	Q65FD5	Q65fd5 bacillus li
174	86.5	6.2	586	2	Q7ZV33	Q7zv33 brachydanio	247	84.5	6.1	408	2	Q7XB13	Q7xb13 tritricum ae
175	86.5	6.2	659	2	Q8MGF7	Q8mgf7 nardostachy	248	84.5	6.1	453	1	TDE2_HUMAN	Q9nrx5 homo sapien
176	86.5	6.2	732	2	Q9TJ08	Q9tj08 chimarrhis	249	84.5	6.1	453	2	Q9RNX3	Q9rnrx3 rhizobium e
177	86.5	6.2	770	2	Q9YC94	Q9yc94 aeropyrum p	250	84.5	6.1	463	2	Q66C42	Q66c42 yersinia ps
										463	2	Q8ZFW8	Q8zfw8 yersinia ps

251	84.5	6.1	473	2	Q65N12	Q65n12 bacillus li	324	82.5	5.9	452	2	Q9ZKR4	Q9zkr4 helicobacte
252	84.5	6.1	479	2	Q65N10	Q65110 oryza sativ	325	82.5	5.9	462	2	Q6F0L1	Q6f0l1 mesoplasma
253	84.5	6.1	479	2	Q9WZ89	Q9wz89 thermotoga	326	82.5	5.9	471	2	Q8SSS9	Q8ss59 lactobacill
254	84.5	6.1	491	2	Q18154	Q18154 caenorhabdi	327	82.5	5.9	478	2	Q8EEL5	Q8eel5 shewanella
255	84.5	6.1	515	2	Q9LN48	Q9ln48 arabadopsi	328	82.5	5.9	486	2	Q82YJ7	Q82yj7 enterococcu
256	84.5	6.1	562	2	Q9FLH8	Q9flh8 arabadopsi	329	82.5	5.9	494	1	N4M_TIRU	Q36834 trichophyto
257	84.5	6.1	589	2	Q95ZV6	Q95zy6 caenorhabdi	330	82.5	5.9	508	2	Q95OR5	Q950r5 spizellomyc
258	84.5	6.1	638	2	Q33749	Q33749 arabacia lix	331	82.5	5.9	543	2	Q7Z517	Q7z517 homo sapien
259	84.5	6.1	702	2	Q9TLF1	Q9tlf1 lindenbergi	332	82.5	5.9	548	2	Q6AAJ7	Q6aa17 propionibac
260	84.5	6.1	820	2	Q45585	Q45585 caenorhabdi	333	82.5	5.9	596	1	AGP2_YEAST	Q38030 saccharomyc
261	84.5	6.1	913	2	Q7UJ14	Q7uj14 rhodospirill	334	82.5	5.9	620	2	Q7SSR8	Q7ss58 neurospora
262	84	6.0	172	2	Q9TA01	Q9ta01 lampetra fl	335	82.5	5.9	623	2	Q8EP35	Q8ep35 rhizobium l
263	84	6.0	234	2	Q99N04	Q99n04 mus musculu	336	82.5	5.9	640	2	Q6MB47	Q6mb47 parachlamyd
264	84	6.0	295	2	Q7YF54	Q7yfs4 neivamyxex	337	82.5	5.9	671	2	Q75113	Q75113 ashbya goss
265	84	6.0	318	2	Q97N11	Q97n11 streptococc	338	82.5	5.9	680	2	Q8SL84	Q8sl84 nardostachy
266	84	6.0	329	2	Q8U0A2	Q8u0a2 pyrococcus	339	82.5	5.9	680	2	Q70SP4	Q70sp4 limosella m
267	84	6.0	403	2	Q7MUU1	Q7muu1 porphyromon	340	82.5	5.9	704	2	Q9SCD0	Q9scd0 gustavia su
268	84	6.0	408	2	Q83MR3	Q83mr3 tropheryma	341	82.5	5.9	733	2	Q8VXB8	Q8vxb8 oryza sativ
269	84	6.0	408	2	Q83N96	Q83n96 tropheryma	342	82.5	5.9	1457	2	Q9HCE0	Q9hce0 homo sapien
270	84	6.0	460	2	Q59186	Q59186 pyrococcus	343	82.5	5.9	2520	2	Q7PPE3	Q7ppe3 anopheles g
271	84	6.0	478	2	Q74F67	Q74f67 geobacter s	344	82	5.9	219	2	Q75250	Q75250 homo sapien
272	84	6.0	492	2	Q7OAL6	Q7gai6 anopheles g	345	82	5.9	267	2	Q88HZ2	Q88hz2 pseudomonas
273	84	6.0	575	2	Q3I642	Q3i642 pseudomonas	346	82	5.9	299	1	T2R3_RAT	Q9jku0 rattus norv
274	84	6.0	597	2	Q9KUN6	Q9kuw6 vibrio chol	347	82	5.9	313	2	Q87GV0	Q87gv0 vibrio para
275	84	6.0	736	2	Q9TJ51	Q9tj51 pauridianth	348	82	5.9	317	2	Q9K6Y6	Q9k6y6 bacillus ha
276	84	6.0	830	2	Q6C772	Q6c772 yarrowia li	349	82	5.9	327	2	Q9KT03	Q9kt03 vibrio chol
277	84	6.0	935	2	Q32P04	Q3zp04 tropaeolum	350	82	5.9	339	2	Q84ET2	Q84et2 uncultured
278	84	6.0	4083	1	DXHC_ASHCO	Q9cim7 ashbya goss	351	82	5.9	356	2	Q9FZ96	Q9fz96 arabadopsi
279	83.5	6.0	261	1	YRBE_HAEIN	P45030 haemophilus	352	82	5.9	359	2	Q9M7R1	Q9m7r1 arabadopsi
280	83.5	6.0	295	2	Q9JVJ1	Q9jvj1 neisseria m	353	82	5.9	359	2	Q97C50	Q97cs0 thermoplas
281	83.5	6.0	324	2	Q8XX91	Q8xx91 ralstonia s	354	82	5.9	389	2	O25590	O25590 helicobacte
282	83.5	6.0	330	2	Q8AA46	Q8aa46 bacteroides	355	82	5.9	405	2	Q983X3	Q983x3 rhizobium l
283	83.5	6.0	333	2	Q8E4D6	Q8e4d6 streptococc	356	82	5.9	446	1	CITN_KLEPN	P31602 klebsiella
284	83.5	6.0	468	2	Q8AX78	Q8axy8 clostridium	357	82	5.9	459	2	Q70XF0	Q70xf0 dromiciops
285	83.5	6.0	509	2	Q8IA95	Q8ia95 caenorhabdi	358	82	5.9	465	2	Q74M77	Q74m77 nanorhachae
286	83.5	6.0	521	1	YJCB_SCHPO	Q74949 saccharomyc	359	82	5.9	488	2	Q93YP9	Q93yp9 arabadopsi
287	83.5	6.0	521	1	Q75B57	Q875s7 saccharomyc	360	82	5.9	494	2	Q6FOR2	Q6for2 mesoplasma
288	83.5	6.0	531	2	Q83EA0	Q83ea0 coxiella bu	361	82	5.9	497	2	Q97A43	Q97a43 thermoplas
289	83.5	6.0	605	2	Q9L1F6	Q9llf6 streptomyce	362	82	5.9	498	2	Q73GM3	Q73gw3 wolbachia p
290	83.5	6.0	638	1	N05M_PARLI	P12776 paracentroc	363	82	5.9	545	2	Q8FNV5	Q8fnv5 corynebacte
291	83.5	6.0	693	2	Q85GD2	Q85gd2 nardostachy	364	82	5.9	548	2	Q9A8F3	Q9a8f3 caulobacter
292	83.5	6.0	736	2	Q9TJ27	Q9tj27 anthosperm	365	82	5.9	557	1	YCQ4_SCHPO	Q4537 schizosacch
293	83.5	6.0	743	2	Q8WH76	Q8wh76 forgesia ra	366	82	5.9	557	2	Q8G3S6	Q8g3s6 bifidobacte
294	83.5	6.0	976	2	Q6FKX5	Q6fkx5 candida gla	367	82	5.9	573	2	Q09932	Q09932 caenorhabdi
295	83.5	6.0	1829	2	Q86HD9	Q86hd9 dictyosteli	368	82	5.9	594	2	Q7T709	Q7t709 citrus tris
296	83	6.0	305	2	Q8YWR6	Q8ywr6 anabaena sp	369	82	5.9	706	2	O45283	O45283 caenorhabdi
297	83	6.0	318	2	Q8DNJ4	Q8dnj4 streptococc	370	82	5.9	748	2	Q6A6C2	Q6a6c2 propionibac
298	83	6.0	321	1	OSV1_HUMAN	Q8ntb5 homo sapien	371	82	5.9	881	2	Q6F8D1	Q6f8d1 acinetobact
299	83	6.0	321	1	Q6NTB5	Q6ntb5 homo sapien	372	82	5.9	884	2	Q8ER30	Q8er30 oceanobacil
300	83	6.0	427	2	Q7P8Q1	Q7p8q1 rickettsia	373	82	5.9	1029	2	Q6KAN9	Q6kan9 mus musculu
301	83	6.0	427	2	Q92HP5	Q92hp5 rickettsia	374	82	5.9	1139	2	Q8ZC91	Q8zcn1 versinia pe
302	83	6.0	457	2	Q8U1E5	Q8ue5 pyrococcus	375	82	5.9	1156	2	Q74WP6	Q74wp6 versinia pe
303	83	6.0	460	2	Q9V0Y7	Q9v0y7 pyrococcus	376	82	5.9	1168	1	CYAC_HUMAN	O43366 homo sapien
304	83	6.0	466	2	Q7VNG8	Q7vng8 haemophilus	377	81.5	5.9	205	2	Q97FC0	Q97pc0 streptococc
305	83	6.0	467	2	Q6F9F8	Q6f9f8 acinetobact	378	81.5	5.9	205	2	Q8CYE9	Q8cye9 streptococc
306	83	6.0	496	2	Q9I4I8	Q9i4i8 pseudomonas	379	81.5	5.9	268	2	Q7MKQ7	Q7mkq7 vibrio vuln
307	83	6.0	587	2	Q87T28	Q87t28 pseudomonas	380	81.5	5.9	268	2	Q8D9M9	Q8d9m9 vibrio vuln
308	83	6.0	637	1	N05M_STRPU	P15552 strongyloce	381	81.5	5.9	292	2	Q92DG0	Q92dgn listeria in
309	83	6.0	802	2	Q8S278	Q8sz78 drosophila	382	81.5	5.9	307	1	UPP2_CLOAB	Q97k6 clostridium
310	83	6.0	1139	2	Q66DQ6	Q66dq6 versinia ps	383	81.5	5.9	321	2	Q94VH0	Q94vhn varanus gou
311	83	6.0	1635	2	Q9C1I7	Q9c1i7 mycosphaere	384	81.5	5.9	325	2	Q973Q6	Q973q6 sulfolobus
312	83	6.0	2159	2	Q8RUQ1	Q8ruq1 zea mays (m	385	81.5	5.9	351	2	Q9FZ95	Q9fz95 arabadopsi
313	83	6.0	2159	2	Q8RVL1	Q8rvl1 zea mays (m	386	81.5	5.9	399	2	Q8NCC4	Q8nc4 homo sapien
314	82.5	5.9	281	2	Q83BV7	Q83bv7 coxiella bu	387	81.5	5.9	435	2	Q88CV8	Q88cv8 pseudomonas
315	82.5	5.9	346	2	Q8TQ84	Q8tq84 methanosarc	388	81.5	5.9	436	2	Q7YZ03	Q7yz03 cryptospori
316	82.5	5.9	368	2	Q72KY8	Q72ky8 thermus the	389	81.5	5.9	438	2	Q9HUD9	Q9hud9 pseudomonas
317	82.5	5.9	391	1	EPT1_YEAST	P22140 saccharomyc	390	81.5	5.9	454	2	Q884R2	Q884r2 pseudomonas
318	82.5	5.9	400	2	Q7M9I6	Q7m9i6 wolinnella s	391	81.5	5.9	454	2	Q89WU1	Q89wu1 bradyrhizob
319	82.5	5.9	418	2	Q8XKM9	Q8xkm9 pseudomonas	392	81.5	5.9	467	2	Q9W1Z2	Q9w1z2 drosophila
320	82.5	5.9	437	2	Q8IKK3	Q8ike3 plasmodium	393	81.5	5.9	485	2	O18063	O18063 caenorhabdi
321	82.5	5.9	439	2	Q8P5I4	Q8p5i4 xanthomonas	394	81.5	5.9	485	2	Q8SYB7	Q8syb7 drosophila
322	82.5	5.9	448	2	Q6DVM4	Q6dvm4 triops long	395	81.5	5.9	485	2	Q9WI23	Q9wi23 drosophila
323	82.5	5.9	451	2	Q82CI8	Q82ci8 streptomyce	396	81.5	5.9	510	2	Q34523	Q34523 fasciola he

397	81.5	5.9	535	2	Q53111	Q53111 rhodobacter	470	80.5	5.8	536	2	Q6MEN5	Q6men5 parachlamyd
398	81.5	5.9	626	2	Q8XUM7	Q8xum7 ralstonia s	471	80.5	5.8	590	1	CAN1_YEAST	P04817 saccharomyc
399	81.5	5.9	711	2	Q6LH73	Q6lh73 photobacter	472	80.5	5.8	637	2	Q21277	Q21277 reclinomona
400	81.5	5.9	713	2	Q9VWG4	Q9vvg4 drosophila	473	80.5	5.8	650	2	Q7FMQ9	Q7fmq9 anopheles g
401	81.5	5.9	724	2	Q8MRAB	Q8mra8 drosophila	474	80.5	5.8	660	2	Q891N8	Q891n8 clostridium
402	81.5	5.9	724	2	Q9TJZ6	Q9tjz6 alseis lugo	475	80.5	5.8	728	2	Q98702	Q98702 luculia gra
403	81.5	5.9	732	2	Q9TJZ6	Q9tjz6 illia trif	476	80.5	5.8	732	2	Q9TJY9	Q9tjy9 calycophyll
404	81.5	5.9	732	2	Q9TJS0	Q9tjs0 pognonopus s	477	80.5	5.8	834	1	NAH3_HUMAN	P48764 homo sapien
405	81.5	5.9	734	2	Q98706	Q98706 chiocecca r	478	80	5.7	226	2	Q81KJ3	Q81kj3 bacillus an
406	81.5	5.9	741	2	Q71QV9	Q71qv9 siegesbecki	479	80	5.7	266	2	Q9HXP7	Q9hxp7 pseudomonas
407	81.5	5.9	855	2	Q6BGA9	Q6bga9 parametium	480	80	5.7	268	2	Q76FP9	Q76fp9 steyla plic
408	81.5	5.9	4960	2	Q7PZB3	Q7pzb3 anopheles g	481	80	5.7	277	2	Q818H6	Q818h6 bacillus ce
409	81	5.8	226	2	Q816R9	Q816r9 bacillus ce	482	80	5.7	285	2	Q6YQJ4	Q6yqj4 onion yello
410	81	5.8	293	1	Y417_CHLTR	Q84422 chlamydia t	483	80	5.7	286	2	Q63CM0	Q63cm0 bacillus ce
411	81	5.8	293	2	Q92WD8	Q92wd8 rhizobium m	484	80	5.7	286	2	Q81RV2	Q81rv2 bacillus an
412	81	5.8	313	1	RBN_VIBVU	Q8dd62 vibrio vuln	485	80	5.7	286	2	Q6HK25	Q6hk25 bacillus th
413	81	5.8	313	1	RBN_VIBVY	Q7mq07 vibrio vuln	486	80	5.7	291	2	Q8UIQ9	Q8uiq9 agrobacteri
414	81	5.8	375	2	P95505	P95505 prochloroth	487	80	5.7	299	2	Q6AL50	Q6al50 desulfotale
415	81	5.8	382	2	Q7P040	Q7pq40 anopheles g	488	80	5.7	322	2	Q9GEH0	Q9geh0 memecylon b
416	81	5.8	382	2	Q918P4	Q9i8p4 cyprinus ca	489	80	5.7	339	2	Q84ET1	Q84et1 prochloroth
417	81	5.8	396	2	Q83KE0	Q83ke0 shigella fl	490	80	5.7	363	2	Q8KX39	Q8kx39 clostridium
418	81	5.8	422	2	Q6ESPS	Q6esp5 oryza sativ	491	80	5.7	391	2	Q6LY81	Q6ly81 methanococc
419	81	5.8	422	2	Q8Y1K4	Q8ylk4 ralstonia s	492	80	5.7	429	1	ARSB_STAAU	P30329 staphylococ
420	81	5.8	438	2	Q8X4U5	Q8x4u5 escherichia	493	80	5.7	429	2	Q9AC73	Q9ac73 staphylococ
421	81	5.8	461	1	YCJJ_ECOLI	P76037 escherichia	494	80	5.7	439	2	Q8PGX4	Q8pgx4 xanthomona
422	81	5.8	479	2	Q87155	Q87155 vibrio chol	495	80	5.7	445	2	Q6NF01	Q6nf01 corynebacte
423	81	5.8	485	2	Q7PQT4	Q7pqt4 anopheles g	496	80	5.7	451	2	Q617X8	Q617x8 leptotyphlo
424	81	5.8	487	2	Q9FRL3	Q9frl3 arabadopsis	497	80	5.7	472	2	Q9N5Q8	Q9n5q8 caenorhabdi
425	81	5.8	515	2	Q8TF71	Q8tf71 homo sapien	498	80	5.7	488	2	Q966D7	Q966d7 caenorhabdi
426	81	5.8	544	1	YRT3_CABEL	Q10046 caenorhabdi	499	80	5.7	516	2	Q94JG1	Q94jg1 oryza sativ
427	81	5.8	548	2	Q8AA29	Q8aa29 bacteroides	500	80	5.7	558	2	Q6XRA4	Q6xra4 uncultured
428	81	5.8	550	2	Q7NZQ0	Q7nzo0 chromobacte	501	80	5.7	657	2	Q6XJM6	Q6xjm6 inhambanell
429	81	5.8	595	2	Q91MW8	Q9imj8 menangle vi	502	80	5.7	671	2	Q7WXB7	Q7wxb7 alcaligenes
430	81	5.8	608	2	Q7QP79	Q7qp79 giardia lam	503	80	5.7	699	2	Q91LF3	Q91lf3 hemaphysma
431	81	5.8	647	2	Q9GEU0	Q9geu0 samolia val	504	80	5.7	702	2	Q19823	Q19823 alsobia sp.
432	81	5.8	657	2	Q6XJ11	Q6xj11 sideroxyylon	505	80	5.7	714	2	Q97Y59	Q97y59 mycobacteri
433	81	5.8	710	2	Q19824	Q19824 cobananthus	506	80	5.7	740	2	Q97JU4	Q97ju4 cephalanthu
434	81	5.8	724	2	Q9GF06	Q9gfo6 jacquinia u	507	80	5.7	740	2	Q8ZQN3	Q8zqn3 salmonella
435	81	5.8	734	2	Q9THV8	Q9thv8 rondeleteia	508	80	5.7	902	2	Q9KX99	Q9kx99 bacillus ha
436	81	5.8	875	2	Q9V8U1	Q9v8u1 drosophila	509	80	5.7	1067	2	Q8S5J8	Q8s5j8 shewanella
437	81	5.8	971	2	Q68XX4	Q68xx4 rickettsia	510	80	5.7	1123	2	Q9LYR7	Q9lyr7 arabadopsis
438	81	5.8	1102	2	Q88CW3	Q88cw3 pseudomonas	511	80	5.7	1480	2	Q6C5L2	Q6c5l2 yarrowia li
439	81	5.8	2187	1	POLG_CXB20	Q9ylg5 c genome po	512	79.5	5.7	234	2	Q61TCS9	Q6jcs9 aleuroplatu
440	80.5	5.8	162	2	Q7NN16	Q7nn16 gloebacter	513	79.5	5.7	264	2	Q61TH2	Q6ith2 cercaria ba
441	80.5	5.8	261	2	Q6LFB2	Q6ltb2 photobacter	514	79.5	5.7	264	2	Q61T11	Q6i11 cercaria ba
442	80.5	5.8	288	2	Q85JA0	Q85ja0 clonorchis	515	79.5	5.7	293	2	Q66D49	Q66d49 yersinia ps
443	80.5	5.8	291	2	Q746X4	Q746x4 geobacter s	516	79.5	5.7	296	2	Q93KC0	Q93kc0 erwania chr
444	80.5	5.8	316	2	Q647F8	Q647f8 thermoprote	517	79.5	5.7	297	2	Q6D417	Q6d417 erwania car
445	80.5	5.8	321	2	Q94VD4	Q94vd4 varanus pan	518	79.5	5.7	297	2	Q7U561	Q7u561 synchococc
446	80.5	5.8	324	2	Q83Z26	Q83z26 lamprocysti	519	79.5	5.7	298	2	Q8R257	Q8r257 mus musculu
447	80.5	5.8	333	2	Q81HX6	Q8inx6 plasmodium	520	79.5	5.7	308	2	Q6CTH9	Q6cth9 kluyveromyc
448	80.5	5.8	334	2	Q81QJ7	Q8iqj7 drosophila	521	79.5	5.7	308	2	Q6ACY4	Q6acy4 leifsonia x
449	80.5	5.8	334	2	Q6AML9	Q6awl9 drosophila	522	79.5	5.7	317	2	Q7UKZ3	Q7ukz3 rhodopirell
450	80.5	5.8	359	2	Q99RB8	Q99rb8 staphylococ	523	79.5	5.7	323	2	Q8DUD9	Q8dud9 streptococc
451	80.5	5.8	359	2	Q792Z9	Q79z29 staphylococ	524	79.5	5.7	384	2	Q88ZD3	Q88zd3 lactobacill
452	80.5	5.8	359	2	Q7A314	Q7a314 staphylococ	525	79.5	5.7	398	2	Q7NVC7	Q7nvc7 chromobacte
453	80.5	5.8	359	2	Q6G6F7	Q6g6f7 staphylococ	526	79.5	5.7	405	2	Q77085	Q77085 caenorhabdi
454	80.5	5.8	366	2	Q8CW25	Q8cw25 streptococc	527	79.5	5.7	443	2	Q95AK6	Q95ak6 dialypetatu
455	80.5	5.8	393	2	Q8CNZ2	Q8cng2 staphylococ	528	79.5	5.7	445	2	Q55937	Q55937 synchocyst
456	80.5	5.8	413	2	Q81NE5	Q81ne5 bacillus an	529	79.5	5.7	445	2	Q6HKB2	Q6hkb2 bacillus th
457	80.5	5.8	433	2	Q66PD9	Q66fd9 yersinia ps	530	79.5	5.7	461	2	Q7UCQ4	Q7ucq4 shigella fl
458	80.5	5.8	433	2	Q74XD2	Q74xd2 yersinia pe	531	79.5	5.7	479	2	Q83RL6	Q83rl6 shigella fl
459	80.5	5.8	433	2	Q8Z1Y7	Q8ziy7 yersinia pe	532	79.5	5.7	485	2	Q73Y55	Q73y55 mycobacteri
460	80.5	5.8	433	2	Q87VV4	Q87vv4 pseudomonas	533	79.5	5.7	499	2	Q9UTP1	Q9utp1 pyrococcus
461	80.5	5.8	446	2	Q951C1	Q951c1 tetrahymena	534	79.5	5.7	505	2	Q93GK1	Q93gk1 bacillus st
462	80.5	5.8	469	2	P93561	P93561 solanum tub	535	79.5	5.7	517	2	Q6MY57	Q6my57 aspergillus
463	80.5	5.8	470	2	Q9CP91	Q9cp91 pasteurella	536	79.5	5.7	522	2	Q7QJ78	Q7qj78 anopheles g
464	80.5	5.8	473	2	Q34718	Q34718 bacillus su	537	79.5	5.7	539	1	FIXN_AGR77	P98055 agrobacteri
465	80.5	5.8	475	2	Q6LR41	Q6lr41 photobacter	538	79.5	5.7	542	2	Q8YBM8	Q8ybm8 brucella me
466	80.5	5.8	523	2	Q8AAX1	Q8aax1 bacteroides	539	79.5	5.7	542	2	Q8RWF3	Q8rfw3 brucella su
467	80.5	5.8	528	2	Q7DDN3	Q7ddn3 neisseria m	540	79.5	5.7	544	2	Q64940	Q64940 avian infec
468	80.5	5.8	528	2	Q9JRD7	Q9jrd7 neisseria m	541	79.5	5.7	570	2	Q8UF62	Q8uf62 agrobacteri
469	80.5	5.8	531	2	Q6KI84	Q6ki84 mycoplasma	542	79.5	5.7	573	2	Q63FV4	Q63fv4 bacillus ce

543	79.5	5.7	573	2	O81V13	Q81V13 bacillus an	616	79	5.7	738	2	Q9TJS8	Q9TJS8 morinda cit
544	79.5	5.7	593	2	O6BM61	Q6bm61 debaryomyce	617	79	5.7	746	2	Q9TLB7	Q9tlb7 digitalis p
545	79.5	5.7	598	2	Q7CZ11	Q7cz11 agrobacteri	618	79	5.7	819	2	Q31582	Q31582 bacillus su
546	79.5	5.7	600	2	Q6LKCO	Q6lkco photobacter	619	79	5.7	1501	2	Q8CQI9	Q8cig9 mus musculu
547	79.5	5.7	613	2	Q8CBQ1	Q8cbq1 mus musculu	620	79	5.7	1521	2	Q8OZZ8	Q8oaz8 mus musculu
548	79.5	5.7	628	2	Q67ML1	Q67ml1 symbiobacte	621	79	5.7	1521	2	Q8CGS3	Q8cgs3 mus musculu
549	79.5	5.7	632	2	Q9A247	Q9az47 enterobacte	622	79	5.7	1521	2	Q8CIP6	Q8cip6 mus musculu
550	79.5	5.7	669	2	Q6USQ3	Q6usc3 valeriana e	623	79	5.7	2198	2	Q18990	Q18990 caenorhabdi
551	79.5	5.7	677	2	Q6CY48	Q6cy48 kluyveromyc	624	78.5	5.6	169	2	Q9HSA7	Q9hsa7 halobacteri
552	79.5	5.7	695	2	Q9TUS9	Q9tj9 musaenda a	625	78.5	5.6	241	1	MCBE_ECOLI	P05528 escherichia
553	79.5	5.7	697	2	Q6YSA9	Q6ysa9 oryza sativ	626	78.5	5.6	242	2	Q6LPC6	Q6lpc6 photobacter
554	79.5	5.7	699	2	Q91YL7	Q91yl7 mus musculu	627	78.5	5.6	264	2	Q6ITH4	Q6ith4 cercaria ba
555	79.5	5.7	741	2	Q32132	Q32132 chrysanthem	628	78.5	5.6	264	2	Q6ITI2	Q6iti2 cercaria ba
556	79.5	5.7	831	1	NAH3_RAT	P26433 rattus norv	629	78.5	5.6	298	2	Q65V25	Q65v25 manihemia
557	79.5	5.7	878	2	Q8MK10	Q8mk10 drosophila	630	78.5	5.6	298	2	Q73T54	Q73t54 mycobacteri
558	79.5	5.7	976	2	Q96VU4	Q96vu4 blumeria gr	631	78.5	5.6	314	2	Q97OC7	Q97oc7 sulfolobus
559	79	5.7	154	2	Q42211	Q42211 necturus ma	632	78.5	5.6	316	2	Q7EY23	Q7ey23 oryza sativ
560	79	5.7	172	1	NU6M_PETMA	Q35544 petromyzon	633	78.5	5.6	320	2	Q9BBU4	Q9bbu4 warnekeia m
561	79	5.7	183	1	Y507_HABIN	P44010 haemophilus	634	78.5	5.6	320	2	Q7ZWS9	Q7zws9 xenopus lae
562	79	5.7	192	2	Q6CYK5	Q6cyk5 erwinia car	635	78.5	5.6	321	2	Q9BBV9	Q9bbv9 mouriri hel
563	79	5.7	226	2	Q6HCD0	Q6hcd0 bacillus th	636	78.5	5.6	325	2	Q9MRZ1	Q9mrz1 heterocentr
564	79	5.7	229	2	Q8XIK9	Q8xik9 clostridium	637	78.5	5.6	330	2	Q9VU64	Q9vu64 drosophila
565	79	5.7	289	2	Q946J9	Q946j9 medicago tr	638	78.5	5.6	340	2	Q8G845	Q8g845 bifidobacte
566	79	5.7	293	1	Y543_CHLPN	Q92809 chlamydia p	639	78.5	5.6	356	2	Q8DTT2	Q8dt2 streptococc
567	79	5.7	293	2	Q9KD25	Q9kd25 bacillus ha	640	78.5	5.6	366	1	YB96_METJA	Q58596 methanococ
568	79	5.7	300	2	Q6HMF1	Q6hm61 bacillus th	641	78.5	5.6	389	2	Q93TD9	Q93td9 pseudomonas
569	79	5.7	307	2	Q9JTQ9	Q9jqt9 neisseria m	642	78.5	5.6	389	2	Q87WD8	Q87wd8 pseudomonas
570	79	5.7	310	2	Q7MJN1	Q7mjn1 vibrio vuln	643	78.5	5.6	393	2	Q639K7	Q639k7 bacillus ce
571	79	5.7	310	2	Q8DAH5	Q8dah5 vibrio vuln	644	78.5	5.6	397	2	Q8K377	Q8kw37 ruegeria sp
572	79	5.7	354	2	Q97C19	Q97c19 thermoplasm	645	78.5	5.6	405	2	Q9U2M5	Q9uzm5 caenorhabdi
573	79	5.7	369	2	Q8PL40	Q8pl40 xanthomonas	646	78.5	5.6	411	2	Q89ZC7	Q89zc7 bacteroides
574	79	5.7	372	2	Q6GIA8	Q6gia8 staphylococ	647	78.5	5.6	412	2	Q99X84	Q99x84 staphylococ
575	79	5.7	373	2	Q8LEH3	Q8lhh3 arabisopsis	648	78.5	5.6	412	2	Q7A856	Q7a856 staphylococ
576	79	5.7	377	2	Q9LXX8	Q9lxx8 arabisopsis	649	78.5	5.6	443	2	Q8ZLW4	Q8zlw4 salmonella
577	79	5.7	381	2	Q6FDD6	Q6fdd6 acinetobact	650	78.5	5.6	447	2	Q6CYN0	Q6cyn0 erwinia car
578	79	5.7	386	2	Q7NCK9	Q7nck9 bacteroides	651	78.5	5.6	464	2	Q979J8	Q979j8 thermoplasm
579	79	5.7	389	2	Q64Q99	Q64q99 bacteroides	652	78.5	5.6	470	2	Q6C8J1	Q6c8j1 yarrowia li
580	79	5.7	390	2	Q9X158	Q9x158 thermotoga	653	78.5	5.6	471	2	Q6AB86	Q6ab86 propionibac
581	79	5.7	395	1	HWEB_ARCFU	Q29750 archaeoglob	654	78.5	5.6	482	2	Q83AQ0	Q83aq0 coxiella bu
582	79	5.7	409	2	Q6E830	Q6e830 potnia glad	655	78.5	5.6	483	2	Q85MF7	Q85mf7 cyrestis th
583	79	5.7	410	1	Y588_BUCAI	P57648 buchnera ap	656	78.5	5.6	487	2	Q9UWE7	Q9uwe7 homo sapien
584	79	5.7	414	2	Q66R30	Q66r30 saccharomyc	657	78.5	5.6	490	2	Q9AWL1	Q9awll oryza sativ
585	79	5.7	429	2	Q63YGH	Q63ygh burkholderi	658	78.5	5.6	493	2	Q9VOT0	Q9vot0 pyrococcus
586	79	5.7	438	2	Q7ACT1	Q7act1 escherichia	659	78.5	5.6	501	2	Q8FB10	Q8fb10 escherichia
587	79	5.7	438	2	Q8FGD5	Q8fgd5 escherichia	660	78.5	5.6	510	2	Q9B8Y2	Q9b8y2 fasciola he
588	79	5.7	443	2	Q6LKM2	Q6lkm2 photobacter	661	78.5	5.6	512	2	Q6ZMD2	Q6zmd2 homo sapien
589	79	5.7	444	2	Q7VT98	Q7vt98 bordetella	662	78.5	5.6	526	2	Q6MUB7	Q6mub7 mycoplasma
590	79	5.7	444	2	Q7W2C1	Q7w2c1 bordetella	663	78.5	5.6	526	2	Q6DCE3	Q6dce3 xenopus lae
591	79	5.7	444	2	Q7WR89	Q7wr89 bordetella	664	78.5	5.6	559	2	Q50465	Q50465 mycobacteri
592	79	5.7	444	2	Q9KKW1	Q9kkw1 vibrio chol	665	78.5	5.6	583	2	Q95OT2	Q95ot2 hyaloraphid
593	79	5.7	446	2	Q6LJ00	Q6l000 picrophilus	666	78.5	5.6	591	2	Q8SXJ9	Q8sxj9 drosophila
594	79	5.7	447	2	Q6GER0	Q6ger0 staphylococ	667	78.5	5.6	591	2	Q9V9U1	Q9v9u1 drosophila
595	79	5.7	453	2	Q9Y888	Q9y888 listeria mo	668	78.5	5.6	622	1	COX1_BACSU	P24010 bacillus su
596	79	5.7	456	2	Q8YH05	Q8yh05 thermoplasm	669	78.5	5.6	624	2	Q9LYR6	Q9lyr6 arabisopsis
597	79	5.7	456	2	Q7PBZ7	Q7pbz7 rickettsia	670	78.5	5.6	652	2	Q9TIX1	Q9tix1 codon schen
598	79	5.7	464	2	Q8RC72	Q8rc72 thermoanaer	671	78.5	5.6	682	2	Q6USQ0	Q6usq0 valeriana c
599	79	5.7	473	2	Q16252	Q16252 caenorhabdi	672	78.5	5.6	691	2	Q93YK5	Q93yk5 brassica na
600	79	5.7	481	2	Q6ZEY5	Q6zey5 burkholderi	673	78.5	5.6	732	2	Q98707	Q98707 musaenda e
601	79	5.7	489	2	Q97EE9	Q97ee9 clostridium	674	78.5	5.6	732	2	Q9RUP6	Q9rjp6 strumphia m
602	79	5.7	497	2	Q7TNN9	Q7tnn9 rattus norv	675	78.5	5.6	744	2	Q32645	Q32645 rogersia suf
603	79	5.7	517	2	Q9XYG3	Q9xyg3 dictyosteli	676	78.5	5.6	779	2	Q6A6U5	Q6a6u5 menyanthes
604	79	5.7	534	2	Q88Z37	Q88z37 lactobacill	677	78.5	5.6	825	2	Q6N215	Q6n215 rhodopseudo
605	79	5.7	595	2	Q837Q4	Q837q4 enterococcu	678	78.5	5.6	825	2	Q92L62	Q92l62 rhizobium m
606	79	5.7	602	2	Q7OXI8	Q7oxi8 rhyncholest	679	78.5	5.6	863	2	Q84W30	Q84w30 arabisopsis
607	79	5.7	658	2	Q6XJH8	Q6xjh8 sideroxylon	680	78.5	5.6	1093	2	Q7RKA2	Q7rka2 plasmodium
608	79	5.7	658	2	Q6XJ72	Q6xj72 sideroxylon	681	78.5	5.6	1289	2	Q64533	Q64533 arabisopsis
609	79	5.7	658	2	Q6XJ10	Q6xj10 nesoluma po	682	78.5	5.6	1325	2	Q64533	Q64533 gallid herp
610	79	5.7	669	1	NU5M_ARATH	P29388 arabidopsis	683	78.5	5.6	2556	2	Q9QH56	Q9qh56 caenorhabdi
611	79	5.7	682	2	Q85U14	Q85u14 oryza sativ	684	78	5.6	158	2	Q9XW23	Q9xcw23 rhizobium l
612	79	5.7	685	2	Q19822	Q19822 alsobia sp.	685	78	5.6	197	2	Q98CZ0	Q98cz0 rhizobium l
613	79	5.7	688	2	Q8M8X1	Q8m8x1 sphenoclea	686	78	5.6	227	2	Q8HMJ0	Q8hmj0 carapus ber
614	79	5.7	692	2	Q9TIW2	Q9tiw2 phacelia ca	687	78	5.6	262	2	Q98A38	Q98a38 rhizobium l
615	79	5.7	723	2	Q35193	Q35193 mus musculu	688	78	5.6	268	2	Q6LZZ9	Q6lzz9 methanococ

689	78	5.6	295	2	Q6P8F8	O6P8f8 xenopus tro	762	77.5	5.6	359	2	Q6GDS8	Q6gds8 staphylococ
690	78	5.6	299	2	Q9QX34	Q9qx34 mus musculus	763	77.5	5.6	363	2	Q9VFU4	Q9vfu4 aeropyrum p
691	78	5.6	307	2	Q9JTR8	Q9jtr8 neisseria m	764	77.5	5.6	367	2	Q67RR1	Q67rr1 symbiobacte
692	78	5.6	327	2	Q974Q0	Q974q0 sulfolobus	765	77.5	5.6	368	2	Q85GB7	Q85gb7 cryptochlad
693	78	5.6	335	1	MRAY_CHILMU	Q9p1g6 chlamydia m	766	77.5	5.6	399	2	Q978I2	Q978i2 thermoplasma
694	78	5.6	338	2	Q9KV69	Q9kv69 streptomyces	767	77.5	5.6	406	2	Q6DNG7	Q6dng7 glycine max
695	78	5.6	340	2	Q7S314	Q7s314 neutospora	768	77.5	5.6	436	2	Q6P6X7	Q6p6x7 brachydanio
696	78	5.6	353	2	Q8Q0J7	Q8q0j7 methanosarc	769	77.5	5.6	443	2	Q8TRL4	Q8trl4 methanosarc
697	78	5.6	366	2	Q85F48	Q85f48 bacillus l1	770	77.5	5.6	448	2	Q9XMU9	Q9xmu9 tetrahymena
698	78	5.6	379	2	Q85L69	Q85l69 chimaerohem	771	77.5	5.6	458	2	Q6CZJ3	Q6czj3 erwinia car
699	78	5.6	382	2	Q921S9	Q921s9 rickettsia	772	77.5	5.6	459	2	Q85UJ5	Q85uj5 coturnix ch
700	78	5.6	388	2	Q9RT25	Q9rt25 deinococcus	773	77.5	5.6	460	2	Q7N370	Q7n370 photorhabdu
701	78	5.6	392	2	Q9ESM5	Q9esm5 rattus norv	774	77.5	5.6	461	2	Q8X7F9	Q8x7f9 escherichia
702	78	5.6	396	2	Q8Z591	Q8z591 salmonella	775	77.5	5.6	464	2	Q916G9	Q916g9 pseudomonas
703	78	5.6	396	2	Q8ZNU7	Q8znu7 salmonella	776	77.5	5.6	477	2	Q7MKV7	Q7mkv7 vibrio vuln
704	78	5.6	408	2	Q81RH3	Q81rh3 bacillus an	777	77.5	5.6	477	2	Q87PF8	Q87pf8 vibrio para
705	78	5.6	409	1	CIW3_MOUSE	Q351l1 mus musculus	778	77.5	5.6	477	2	Q8D9I1	Q8d9i1 vibrio vuln
706	78	5.6	409	2	Q6H2P9	Q6h2p9 bacillus an	779	77.5	5.6	479	2	Q7AEJ3	Q7aej3 escherichia
707	78	5.6	409	2	Q6HJQ7	Q6hjqt bacillus th	780	77.5	5.6	492	2	Q7VFT5	Q7vft5 helicobacte
708	78	5.6	411	1	CIW3_RAT	O549i2 rattus norv	781	77.5	5.6	499	2	Q8Z3S3	Q8z3s3 salmonella
709	78	5.6	414	1	YMR7_YEAST	Q04835 saccharomyc	782	77.5	5.6	504	2	Q688L6	Q688l6 oryza sativ
710	78	5.6	416	2	Q6VMS3	Q6vms3 mus musculus	783	77.5	5.6	507	2	Q7VSO9	Q7vsg9 bordetella
711	78	5.6	424	2	Q6SPZ8	Q6sfz8 uncultured	784	77.5	5.6	507	2	Q7WDH8	Q7wdh8 bordetella
712	78	5.6	428	2	Q6LS34	Q6ls34 photobacter	785	77.5	5.6	510	1	Y382_RICPR	Q9zde9 rickettsia
713	78	5.6	452	2	Q7VAQ3	Q7vaq3 prochloroco	786	77.5	5.6	510	2	Q9LE20	Q9le20 arabidopsis
714	78	5.6	462	2	Q9Y8L1	Q9y8l1 pyrococcus	787	77.5	5.6	513	2	Q9KLS4	Q9kls4 vibrio chol
715	78	5.6	467	2	Q95JD3	Q95jd3 cryotolagus	788	77.5	5.6	520	2	Q32477	Q32477 justicia am
716	78	5.6	474	2	Q8GGM7	Q8ggm7 streptomyces	789	77.5	5.6	526	2	Q81501	Q81501 arabidopsis
717	78	5.6	486	2	Q8EKR6	Q8ekr6 shewanella	790	77.5	5.6	531	2	Q6YQU3	Q6yqu3 onion yello
718	78	5.6	486	2	Q687I4	Q687i4 mus musculus	791	77.5	5.6	532	1	COX1_RHOCA	P98059 rhodobacter
719	78	5.6	490	2	Q8FP18	Q8fp18 corynebacte	792	77.5	5.6	535	2	Q55577	Q55577 synchocyst
720	78	5.6	495	2	Q6R914	Q6r914 zea mays (m	793	77.5	5.6	612	2	Q76HH6	Q76hh6 katauoncus
721	78	5.6	498	2	Q8BV50	Q8bv50 mus musculus	794	77.5	5.6	612	2	Q8SUE1	Q8sue1 eutymnus a
722	78	5.6	517	2	Q98H22	Q98h22 rhizobium l	795	77.5	5.6	617	2	Q7S080	Q7s080 neurospora
723	78	5.6	538	2	Q9JAE1	Q9jael mumps virus	796	77.5	5.6	630	1	S6A4_MACMU	Q9mxy0 macaca mula
724	78	5.6	551	2	Q8BWC6	Q8bwg6 m mus muscu	797	77.5	5.6	635	2	Q9ASS7	Q9ase7 arabidopsis
725	78	5.6	553	2	Q6CQ66	Q6cq66 kluyveromyc	798	77.5	5.6	639	2	Q85L86	Q85l86 pisaster oc
726	78	5.6	554	2	Q6NAP5	Q6nap5 rhodospseudo	799	77.5	5.6	648	2	Q8SLR2	Q8slr2 couroupita
727	78	5.6	565	2	Q9F3S8	Q9f3s8 rhodothermu	800	77.5	5.6	649	2	Q28449	Q28449 archaeoglob
728	78	5.6	573	2	Q72LX4	Q72lx4 leptospira	801	77.5	5.6	660	2	Q6Y1T3	Q6y1t3 lachnanthes
729	78	5.6	574	2	Q72T06	Q72t06 leptospira	802	77.5	5.6	665	2	Q9GGT9	Q9ggt9 dultichum a
730	78	5.6	574	2	Q8F2F8	Q8f2f8 leptospira	803	77.5	5.6	693	2	Q96MV6	Q96mv6 homo sapien
731	78	5.6	658	2	Q6XJL1	Q6xjl1 neolemonnie	804	77.5	5.6	695	2	Q97A18	Q97a18 thermoplasma
732	78	5.6	694	2	Q95677	Q95677 solanum dul	805	77.5	5.6	698	2	Q6BGZ2	Q6bgz2 debaryomyces
733	78	5.6	701	2	Q01843	Q01843 caenorhabdi	806	77.5	5.6	699	2	Q7YM04	Q7ym04 metternichi
734	78	5.6	830	2	Q8PQA8	Q8pqa8 xanthomonas	807	77.5	5.6	706	2	Q6MK05	Q6mk05 bdellovibri
735	78	5.6	834	2	Q8E9A7	Q8e9a7 shewanella	808	77.5	5.6	717	1	PAL2_ARATH	P45724 arabidopsis
736	77.5	5.6	212	2	Q9KAJ4	Q9kaj4 bacillus ha	809	77.5	5.6	717	2	Q8RWP4	Q8rwp4 arabidopsis
737	77.5	5.6	243	2	Q93RC4	Q93rc4 escherichia	810	77.5	5.6	744	2	Q8N261	Q8n261 homo sapien
738	77.5	5.6	260	2	Q7VVJ38	Q7vvj38 bordetella	811	77.5	5.6	750	2	Q93S90	Q93s90 xanthomonas
739	77.5	5.6	260	2	Q7W0U7	Q7w0u7 bordetella	812	77.5	5.6	839	2	Q8TQ74	Q8tg74 methanosarc
740	77.5	5.6	260	2	Q7WN67	Q7wn67 bordetella	813	77.5	5.6	855	2	Q75AV9	Q75av9 ashbya goss
741	77.5	5.6	268	2	Q8U2B7	Q8u2b7 pyrococcus	814	77.5	5.6	861	2	Q89FW4	Q89fw4 bradyrhizob
742	77.5	5.6	283	2	Q92WH1	Q92wh1 rhizobium m	815	77.5	5.6	870	2	Q8N639	Q8n639 homo sapien
743	77.5	5.6	287	2	Q6NJG1	Q6njg1 corynebacte	816	77.5	5.6	870	2	Q7Z3F1	Q7z3f1 homo sapien
744	77.5	5.6	288	2	Q9MFR1	Q9mf61 beta vulgar	817	77.5	5.6	945	2	Q6FG02	Q6fg02 acinetobact
745	77.5	5.6	288	2	Q9M4S9	Q9m4s9 allium cepa	818	77.5	5.6	953	1	CW43_YEAST	P25618 saccharomyc
746	77.5	5.6	291	2	Q8ASD9	Q8asd9 desulfocale	819	77.5	5.6	1118	2	Q9HUE7	Q9hue7 pseudomonas
747	77.5	5.6	292	2	Q8Y8N6	Q8y8n6 listeria mo	820	77.5	5.6	1402	1	Y232_HUMAN	Q92828 homo sapien
748	77.5	5.6	292	2	Q721V7	Q721v7 listeria mo	821	77	5.5	181	2	Q8ZU94	Q8zu94 pyrobaculum
749	77.5	5.6	293	2	Q8ZGV5	Q8zgv5 versinia pe	822	77	5.5	262	2	Q8KJ17	Q8kj17 rhizobium l
750	77.5	5.6	293	2	Q88E98	Q88e98 pseudomonas	823	77	5.5	269	2	Q73K03	Q73k03 treponema d
751	77.5	5.6	296	2	Q92ZHO	Q92zh0 rhizobium m	824	77	5.5	277	2	Q73Q06	Q73q06 bacillus ce
752	77.5	5.6	308	2	Q860J1	Q860j1 borrelia ga	825	77	5.5	282	2	Q8Y7M2	Q8y7m2 listeria mo
753	77.5	5.6	312	2	Q8VG20	Q8vg20 mus musculus	826	77	5.5	282	2	Q720H2	Q720h2 listeria mo
754	77.5	5.6	312	2	Q7TR57	Q7tr57 mus musculus	827	77	5.5	284	2	Q21311	Q21311 tetrahymena
755	77.5	5.6	313	2	Q7TS53	Q7ts53 mus musculus	828	77	5.5	284	2	Q9T7M5	Q9t7m5 tetrahymena
756	77.5	5.6	317	2	Q8RFJ5	Q8rfj5 fusobacteri	829	77	5.5	286	2	Q739X4	Q739x4 bacillus ce
757	77.5	5.6	318	1	NUJM_VARRU	Q94vc3 varanus rud	830	77	5.5	293	2	Q82S88	Q82s88 nitrosomona
758	77.5	5.6	321	2	Q94VJ2	Q94vj2 varanus g9	831	77	5.5	295	2	Q7YFS2	Q7yfs2 neivamyrmex
759	77.5	5.6	327	2	Q9MR26	Q9mr26 comolia cor	832	77	5.5	295	2	Q7YFS6	Q7yfs6 nomamyrmex
760	77.5	5.6	335	2	Q9XON3	Q9xon3 thermotoga	833	77	5.5	300	2	Q81TX5	Q81tx5 bacillus an
761	77.5	5.6	347	2	Q70RW1	Q70rw1 berardius b	834	77	5.5	302	2	Q61TX5	Q61tx5 bacillus an

835	77	5.5	310	2	Q89YL4	Q89YL4 bacteroides	908	76.5	5.5	312	2	Q6PC57	O6pc57 brachydanio
836	77	5.5	314	2	Q7TRY1	Q7try1 mus musculus	909	76.5	5.5	316	2	Q6JLH4	O7jll4 caenorhabdi
837	77	5.5	321	2	Q94VE3	Q94ve3 varanus mer	910	76.5	5.5	319	2	Q6Q7V6	O6q7v6 eriocnema f
838	77	5.5	332	2	Q92UP3	Q92up3 rhizobium m	911	76.5	5.5	319	2	Q9YH55	Q9yh55 gallus gall
839	77	5.5	352	2	Q93SN1	Q93sn1 bradyrhizob	912	76.5	5.5	321	2	Q94VD1	Q94vd1 varanus pan
840	77	5.5	352	2	Q9W6K3	Q9w6k3 anolis caro	913	76.5	5.5	321	2	Q9GEG8	Q9geh7 heterocentr
841	77	5.5	353	2	Q9TE65	Q9te65 thalassione	914	76.5	5.5	326	2	Q9GEG7	Q9geh7 heterocentr
842	77	5.5	354	2	Q6F2N6	Q6f2n6 oryza sativ	915	76.5	5.5	327	2	Q8DLE0	Q8dle0 synechococc
843	77	5.5	355	2	Q88DH5	Q88dh5 pseudomonas	916	76.5	5.5	333	2	Q9MRX5	Q9mrx5 tibouchina
844	77	5.5	361	2	Q86JW2	Q86jw2 dictyosteli	917	76.5	5.5	334	2	Q9V056	Q9v056 pyrococcus
845	77	5.5	372	2	Q6DA40	Q6da40 erwinia car	918	76.5	5.5	339	2	Q7U8B3	Q7u8b3 synechococc
846	77	5.5	387	2	Q89I16	Q89i16 bradyrhizob	919	76.5	5.5	339	2	Q7VCR6	Q7vcr6 prochloroco
847	77	5.5	390	2	Q7N821	Q7n821 photorhabd	920	76.5	5.5	344	1	TA10_RAT	Q923y0 rattus norv
848	77	5.5	403	2	Q9HIJ3	Q9hij3 thermoplasm	921	76.5	5.5	353	2	Q9TE67	Q9te67 rhizosoleni
849	77	5.5	417	2	Q97YX9	Q97yx9 sulfolobus	922	76.5	5.5	361	2	Q8AV37	Q8av37 gallus gall
850	77	5.5	438	1	SHIA_ECOLI	P76350 escherichia	923	76.5	5.5	369	2	Q8G6D1	Q8g6d1 bifidobacte
851	77	5.5	438	2	Q34739	Q34739 bacillus su	924	76.5	5.5	370	2	Q8YH19	Q8yh19 bruceila me
852	77	5.5	451	2	Q73GR0	Q73gr0 wolbachia p	925	76.5	5.5	370	2	Q8FXZ1	Q8fxz1 bruceila su
853	77	5.5	459	2	Q8SFC7	Q8sfc7 arenaria in	926	76.5	5.5	382	2	Q85187	Q85187 vibrio chol
854	77	5.5	460	2	Q87GT8	Q87gt8 vibrio para	927	76.5	5.5	385	2	Q81231	Q81z31 homo sapien
855	77	5.5	461	2	Q73JZ7	Q73jz7 treponema d	928	76.5	5.5	388	2	Q9N4S1	Q9n4s1 caenorhabdi
856	77	5.5	471	2	Q97U43	Q97u43 sulfolobus	929	76.5	5.5	395	2	Q8Z700	Q8z700 salmonella
857	77	5.5	476	2	Q7T3R8	Q7t3r8 fugu rubrip	930	76.5	5.5	395	2	Q8ZFI5	Q8zpf5 salmonella
858	77	5.5	478	2	Q91WN3	Q91wn3 mus musculus	931	76.5	5.5	396	2	Q9XDR1	Q9xdri actinobacil
859	77	5.5	485	2	Q87JL4	Q87jl4 vibrio para	932	76.5	5.5	399	2	Q74HG7	Q74hg7 lactobacill
860	77	5.5	486	2	Q6FLH2	Q6flh2 candida gla	933	76.5	5.5	404	2	Q81E11	Q81e11 bacillus ce
861	77	5.5	486	2	Q6G4T8	Q6g4t8 bartonella	934	76.5	5.5	419	2	Q638Y3	Q638y3 bacillus ce
862	77	5.5	506	2	Q80XM3	Q80xm3 mus musculus	935	76.5	5.5	424	2	Q74M02	Q74m02 lactobacill
863	77	5.5	519	1	SC59_YEAST	P20048 saccharomyc	936	76.5	5.5	431	2	Q9K7K1	Q9k7k1 bacillus ha
864	77	5.5	532	2	Q88CD0	Q88cd0 pseudomonas	937	76.5	5.5	443	2	Q71XS7	Q71xs7 listeria mo
865	77	5.5	536	2	Q8KJN9	Q8kjin9 rhizobium l	938	76.5	5.5	450	2	Q7QM18	Q7qmi8 anopheles g
866	77	5.5	540	2	Q82SN0	Q82sn0 nitrosomona	939	76.5	5.5	466	2	Q74HI0	Q74hi0 lactobacill
867	77	5.5	551	1	FIXN_AZOCA	P98056 azorhizobiu	940	76.5	5.5	474	1	PNTB_HAEIN	P43010 haemophilus
868	77	5.5	552	2	Q73V35	Q73v35 mycobacteri	941	76.5	5.5	475	1	HUTN_BACSU	P42087 bacillus su
869	77	5.5	552	2	Q81B60	Q81b60 bacillus ce	942	76.5	5.5	480	2	Q8ERF0	Q8err0 oceanobacil
870	77	5.5	579	2	Q8YSW1	Q8ysw1 anabaena sp	943	76.5	5.5	486	2	Q8MPU6	Q8mpu6 caenorhabdi
871	77	5.5	580	2	Q7PVG5	Q7pvg5 anopheles g	944	76.5	5.5	495	2	Q6E7F5	Q6e7f5 yersinia ps
872	77	5.5	588	2	Q6ALD0	Q6ald0 desulfotale	945	76.5	5.5	495	2	Q8ZBT3	Q8zbt3 yersinia pe
873	77	5.5	597	2	Q6CLN4	Q6cln4 kluyveromyc	946	76.5	5.5	497	2	Q9HL81	Q9hl81 thermoplasm
874	77	5.5	625	2	Q65DA4	Q65da4 bacillus li	947	76.5	5.5	498	2	Q8P1I0	Q8p1i0 streptococc
875	77	5.5	662	1	CYOB_EUCAI	P57543 buchnera ap	948	76.5	5.5	498	2	Q9A0F5	Q9a0f5 streptococc
876	77	5.5	672	2	Q6G0V1	Q6g0v1 bartonella	949	76.5	5.5	498	2	Q8K803	Q8k803 streptococc
877	77	5.5	679	2	Q6H9F9	Q6h9f9 lancea tibe	950	76.5	5.5	515	2	Q645E7	Q645e7 oedipina po
878	77	5.5	695	2	Q7YM01	Q7ym01 vestia lyci	951	76.5	5.5	518	2	Q6CLG6	Q6clg6 kluyveromyc
879	77	5.5	710	2	Q19239	Q19239 caenorhabdi	952	76.5	5.5	541	1	AAP2_NEUCR	O59942 neutrospora
880	77	5.5	716	2	Q9VXB0	Q9vxb0 oryza sativ	953	76.5	5.5	548	2	Q9YBH5	Q9ybh5 aeropyrum p
881	77	5.5	725	2	Q8TJF9	Q8tjf9 spermacoce	954	76.5	5.5	568	2	Q6PML9	Q6pml9 homo sapien
882	77	5.5	731	2	Q8MA29	Q8ma29 cyclocheilo	955	76.5	5.5	568	2	Q9Y6R2	Q9y6r2 homo sapien
883	77	5.5	739	2	Q32109	Q32109 conyza sp.	956	76.5	5.5	568	2	Q8VYR9	Q8vyr9 arabidopsis
884	77	5.5	749	2	Q83812	Q83812 treponema p	957	76.5	5.5	583	2	Q722T4	Q722t4 listeria mo
885	77	5.5	778	2	Q852J4	Q852j4 oryza sativ	958	76.5	5.5	607	2	Q71N57	Q71n57 androsace s
886	77	5.5	785	1	POT5_ARATH	Q9m7k4 arabidopsis	959	76.5	5.5	626	2	Q94243	Q94243 caenorhabdi
887	77	5.5	808	2	Q35190	Q35190 mus musculus	960	76.5	5.5	626	2	Q8CMP0	Q8cmp0 staphylococ
888	77	5.5	907	2	Q92P26	Q92p26 arabidopsis	961	76.5	5.5	630	1	S6A4_CAVPO	Q35899 cavia porce
889	77	5.5	915	2	Q9S7V7	Q9s7v7 arabidopsis	962	76.5	5.5	631	2	Q8HUU2	Q8huu2 bessera tui
890	77	5.5	1138	2	Q96Y88	Q96y88 arabidopsis	963	76.5	5.5	640	2	Q9GEU2	Q9geu2 bessera tui
891	77	5.5	1176	2	Q8F749	Q8f749 acinetobact	964	76.5	5.5	661	2	Q9LBY2	Q9lby2 shewanella
892	77	5.5	1240	2	Q8DK68	Q8dk68 synechococc	965	76.5	5.5	666	2	Q52732	Q52732 rhizobium e
893	77	5.5	1406	2	Q9FN44	Q9fn44 arabidopsis	966	76.5	5.5	669	2	Q8HU33	Q8huu3 milla biflo
894	76.5	5.5	152	2	Q9YDP6	Q9ydp6 aeropyrum p	967	76.5	5.5	672	2	Q8HUU3	Q8huu3 bessera ele
895	76.5	5.5	175	2	Q81J70	Q81jt0 plasmodium	968	76.5	5.5	673	2	Q8HUT0	Q8hut0 dandya thad
896	76.5	5.5	243	2	Q8ZU92	Q8zu92 pyrobaculum	969	76.5	5.5	675	2	Q8HUS1	Q8hus1 muilla clev
897	76.5	5.5	259	2	Q30572	Q30572 ginglymoeto	970	76.5	5.5	677	2	Q6R3K6	Q6r3k6 arabidopsis
898	76.5	5.5	262	1	CITE2_HUMAN	Q8nm3 homo sapien	971	76.5	5.5	683	2	Q34302	Q34302 rhizobium e
899	76.5	5.5	269	2	P96581	P96581 bacillus su	972	76.5	5.5	696	2	Q9TIV2	Q9tiv2 pholistoma
900	76.5	5.5	284	1	FOCA_HAEIN	P43756 haemophilus	973	76.5	5.5	705	2	Q9GHQ1	Q9ghq1 pseudonemac
901	76.5	5.5	289	2	Q22541	Q22541 oryza sativ	974	76.5	5.5	716	2	Q6N428	Q6n428 rhodopsuado
902	76.5	5.5	300	1	YIIP_ECOLI	P32159 escherichia	975	76.5	5.5	724	2	Q6FE05	Q6fe05 acinetobact
903	76.5	5.5	301	2	Q23340	Q23340 caenorhabdi	976	76.5	5.5	725	1	YGL4_YEAST	P53134 saccharomyc
904	76.5	5.5	301	2	Q9KSV5	Q9ksv5 vibrio chol	977	76.5	5.5	729	2	Q8HTN8	Q8htn8 cocculus ca
905	76.5	5.5	305	2	Q9KFT1	Q9kft1 bacillus ha	978	76.5	5.5	734	2	Q96ND6	Q96nd6 homo sapien
906	76.5	5.5	311	1	PAQ3_MOUSE	Q6tcg8 mus musculus	979	76.5	5.5	734	2	Q9TJ73	Q9tj73 guettarda u
907	76.5	5.5	311	2	Q6AXP7	Q6axp7 rattus norv	980	76.5	5.5	745	2	Q8WH81	Q8wh81 escallonia

981	76.5	5.5	745	2	Q8WH88	Q8wh88	escallonia	1054	76	5.5	492	2	Q6FEH2	Q6feh2	acinetobact
982	76.5	5.5	745	2	Q8WH91	Q8wh91	escallonia	1055	76	5.5	494	2	Q6FCQ9	Q6fcq9	acinetobact
983	76.5	5.5	745	2	Q9MTH0	Q9mth0	escallonia	1056	76	5.5	495	2	Q8HCP7	Q8hcp7	oryza sativ
984	76.5	5.5	746	2	Q311H7	Q311h7	schlechtend	1057	76	5.5	495	2	Q6D831	Q6d831	erwinia car
985	76.5	5.5	803	2	Q9N978	Q9n978	leishmania	1058	76	5.5	497	2	QUJ380	Q7u380	bordetella
986	76.5	5.5	811	2	Q84WS3	Q84ws3	oryza sativ	1059	76	5.5	502	1	ACH7_CHICK	P22770	gallus gall
987	76.5	5.5	823	2	Q649F7	Q649f7	uncultured	1060	76	5.5	502	1	NU2C_MESVI	Q9muq6	mesostigma
988	76.5	5.5	855	2	Q9L2T7	Q9l2t7	arabidopsis	1061	76	5.5	509	2	Q643C9	Q643c9	streptomyce
989	76.5	5.5	1342	1	FTSK_EC057	Q8x5h9	escherichia	1062	76	5.5	514	2	Q9CPB6	Q9cpb6	pasteurella
990	76.5	5.5	2967	2	Q41892	Q41892	hepatitis g	1063	76	5.5	518	2	Q6FLP3	Q6flp3	candida gla
991	76	5.5	210	2	Q701X2	Q701x2	uncultured	1064	76	5.5	520	2	Q82WY7	Q82wy7	nitrosomona
992	76	5.5	226	2	Q632U0	Q632u0	baecillus ce	1065	76	5.5	536	2	Q989I2	Q989i2	rhizobium l
993	76	5.5	261	1	ZNUB_HABIN	P44691	haemophilus	1066	76	5.5	551	2	Q76W72	Q76w72	mus musculu
994	76	5.5	275	2	Q97K81	Q97k81	clostridium	1067	76	5.5	554	2	Q89DA3	Q89da3	bradyrhizob
995	76	5.5	275	2	Q89LM8	Q89lm8	clostridium	1068	76	5.5	558	1	CX1B_PARDE	P98002	paracoccus
996	76	5.5	277	2	Q634Q7	Q634q7	baecillus ce	1069	76	5.5	570	1	T7S3_HUMAN	P98093	homo sapien
997	76	5.5	277	2	Q81LV5	Q81lv5	baecillus ce	1070	76	5.5	573	2	Q6HNC4	Q6hnc4	baecillus th
998	76	5.5	277	2	Q6HDN7	Q6hdn7	baecillus th	1071	76	5.5	574	2	Q8DGC1	Q8dgc1	synecococc
999	76	5.5	281	2	Q92CF3	Q92cf3	listeria in	1072	76	5.5	578	2	Q33024	Q33024	ruellia cil
1000	76	5.5	282	2	Q92180	Q92i80	listeria in	1073	76	5.5	580	2	Q85JB7	Q85jb7	harpochytri
1001	76	5.5	282	2	Q9CK77	Q9ck77	pasteurella	1074	76	5.5	612	2	Q94T23	Q94t23	percopsis t
1002	76	5.5	286	2	Q81EN8	Q81en8	baecillus ce	1075	76	5.5	617	2	Q45325	Q45325	caenorhabdi
1003	76	5.5	287	2	Q49874	Q49874	lupinus alb	1076	76	5.5	622	2	Q9HEL3	Q9hel3	neurospora
1004	76	5.5	295	2	Q7YFS9	Q7yfs9	labidus coe	1077	76	5.5	644	2	Q9GEW8	Q9gew8	manilkara z
1005	76	5.5	299	2	Q87JX9	Q87jx9	vibrio para	1078	76	5.5	648	2	Q9GEW8	Q9gew8	manilkara z
1006	76	5.5	312	2	Q912C1	Q912c1	mus musculu	1079	76	5.5	656	2	Q639D7	Q639d7	baecillus ce
1007	76	5.5	316	2	Q8QR03	Q8qr03	pongine her	1080	76	5.5	658	2	Q6XJM3	Q6xjm3	lecomtodoxa
1008	76	5.5	318	2	Q8CN93	Q8cn93	staphylococ	1081	76	5.5	659	2	Q6CAT5	Q6cat5	yarrowia li
1009	76	5.5	321	2	Q6SL25	Q6sl25	argulus ame	1082	76	5.5	659	2	Q8XBE6	Q8xbe6	escherichia
1010	76	5.5	325	2	Q81QX1	Q81qx1	drosophila	1083	76	5.5	663	2	Q6CW54	Q6cw54	kluveromyc
1011	76	5.5	328	2	Q9GEH9	Q9geh9	dichaetanthe	1084	76	5.5	686	2	Q80WJ2	Q80wj2	mus musculu
1012	76	5.5	336	2	Q21716	Q21716	caenorhabdi	1085	76	5.5	695	2	Q32508	Q32508	lycium cest
1013	76	5.5	347	2	Q9VWK6	Q9vwk6	drosophila	1086	76	5.5	699	2	Q9SCG5	Q9scg5	clavija int
1014	76	5.5	353	2	Q9TE69	Q9te69	fragilaria	1087	76	5.5	708	2	Q9THW7	Q9thw7	lytrasacme
1015	76	5.5	356	2	Q8D717	Q8d717	vibrio vuln	1088	76	5.5	719	2	Q6EMC0	Q6emc0	lycopersico
1016	76	5.5	361	2	Q7NP26	Q7np26	chromobacte	1089	76	5.5	724	2	Q7YX45	Q7yx45	caenorhabdi
1017	76	5.5	365	2	Q9KS99	Q9ks99	vibrio chol	1090	76	5.5	738	2	Q8COP3	Q8cop3	mus musculu
1018	76	5.5	371	1	YB2X_HABIN	Q86233	haemophilus	1091	76	5.5	743	2	Q9N2R1	Q9n2r1	drosophila
1019	76	5.5	373	2	Q6FDT2	Q6fdt2	acinetobact	1092	76	5.5	774	2	Q80WJ3	Q80wj3	mus musculu
1020	76	5.5	381	2	Q715Y5	Q715y5	baismys tay	1093	76	5.5	852	2	Q35192	Q35192	mus musculu
1021	76	5.5	384	2	Q6FS89	Q6fs89	candida gla	1094	76	5.5	869	2	Q7Q103	Q7q103	anopheles g
1022	76	5.5	400	2	Q812J4	Q812j4	baecillus ce	1095	76	5.5	904	1	COPP_RAT	Q35142	rattus norv
1023	76	5.5	400	2	Q83NP3	Q83np3	tropheryma	1096	76	5.5	956	2	Q18129	Q18129	caenorhabdi
1024	76	5.5	411	2	Q9XNZ5	Q9xnz5	chelonus sp	1097	76	5.5	958	2	Q8ZFM4	Q8zfm4	versinia pe
1025	76	5.5	415	2	Q88A33	Q88a33	pseudomonas	1098	76	5.5	966	2	Q7PAP6	Q7pap6	caenorhabdi
1026	76	5.5	418	2	Q915T3	Q915t3	pseudomonas	1099	76	5.5	966	2	Q92JFC3	Q92jc3	rickettsia
1027	76	5.5	418	2	Q6BYU7	Q6byu7	debaromyces	1100	76	5.5	971	2	Q9ZE42	Q9ze42	rickettsia
1028	76	5.5	422	1	NAH2_METJA	Q58916	methanococ	1101	76	5.5	1052	1	YLD4_SCHPO	Q42656	schizosacch
1029	76	5.5	424	2	Q81FQ3	Q81f43	baecillus ce	1102	76	5.5	1074	1	EMBC_MYCSM	Q50393	mycobacteri
1030	76	5.5	429	2	Q6GT24	Q6gi24	staphylococ	1103	76	5.5	1165	1	CYA6_MOUSE	Q01341	mus musculu
1031	76	5.5	430	2	Q6Y0P0	Q6y0p0	staphylococ	1104	76	5.5	1241	2	Q9U144	Q9u144	leishmania
1032	76	5.5	430	2	Q6Y0P3	Q6y0p3	staphylococ	1105	76	5.5	1366	2	Q80WJ6	Q80wj6	mus musculu
1033	76	5.5	430	2	Q62B98	Q62b98	burkholderi	1106	76	5.5	1366	2	Q6WGM8	Q6wgm8	lotium mult
1034	76	5.5	430	2	Q63NH2	Q63nh2	burkholderi	1107	76	5.5	1306	2	Q7RSL8	Q7rsl8	plasmodium
1035	76	5.5	431	2	Q6LW64	Q6lw64	lactobacill	1108	75.5	5.4	210	2	Q64625	Q64625	arabidopsis
1036	76	5.5	432	2	Q6L9W3	Q6l9w3	eucalanus b	1109	75.5	5.4	210	2	Q64625	Q64625	arabidopsis
1037	76	5.5	433	2	Q92M74	Q92m74	rhizobium m	1110	75.5	5.4	233	2	Q82JZ0	Q82jz0	salmonella
1038	76	5.5	443	2	Q76W71	Q76m71	mus musculu	1111	75.5	5.4	237	2	Q8X803	Q8x803	escherichia
1039	76	5.5	444	1	QFSP_PETMA	Q42490	petromyzon	1112	75.5	5.4	240	2	Q9ZM55	Q9zm55	helicobacte
1040	76	5.5	447	2	Q9HP02	Q9hpq2	halobacteri	1113	75.5	5.4	252	2	Q31370	Q31370	brachydanio
1041	76	5.5	452	1	TVR1_YEAST	P20049	saccharomyc	1114	75.5	5.4	252	2	Q6SHH1	Q6shh1	uncultured
1042	76	5.5	452	2	Q6SPF4	Q6spf4	uncultured	1115	75.5	5.4	267	2	Q72CM0	Q72cm0	desulfovibr
1043	76	5.5	453	2	Q72LH6	Q72lh6	listeria mo	1116	75.5	5.4	275	2	Q648G2	Q648g2	uncultured
1044	76	5.5	457	2	Q7VUN3	Q7vum3	bordetella	1117	75.5	5.4	295	2	Q7YFS8	Q7yfs8	labidus spi
1045	76	5.5	457	2	Q7W122	Q7w122	bordetella	1118	75.5	5.4	295	2	Q931B9	Q931b9	staphylococ
1046	76	5.5	457	2	Q7W0X0	Q7wgx0	bordetella	1119	75.5	5.4	295	2	Q53619	Q53619	staphylococ
1047	76	5.5	459	2	Q8W9B5	Q8w9b5	vombatus ur	1120	75.5	5.4	296	2	Q9HV25	Q9hv25	pseudomonas
1048	76	5.5	460	2	Q8HM18	Q8hm18	calophryne	1121	75.5	5.4	297	2	Q66E61	Q66e61	versinia ps
1049	76	5.5	461	2	Q7QJ38	Q7qj38	anopheles g	1122	75.5	5.4	297	2	Q82BU5	Q82bu5	versinia pe
1050	76	5.5	467	2	Q6WRY0	Q6wry0	xenopus tro	1123	75.5	5.4	298	2	Q8KPE7	Q8kpe7	bartonella
1051	76	5.5	470	2	Q8FAH1	Q8fah1	escherichia	1124	75.5	5.4	300	2	Q7UB82	Q7ub82	shigella fl
1052	76	5.5	479	2	Q87134	Q87134	vibrio chol	1125	75.5	5.4	300	2	Q8ERA7	Q8era7	oceanobacil
1053	76	5.5	480	2	Q9I2N9	Q9i2n9	pseudomonas	1126	75.5	5.4	305	2	Q6N132	Q6n132	rhodopseudo

1127	75.5	5.4	306	2	Q83PD6	Q83pd6 shigella fl
1128	75.5	5.4	312	2	Q82N48	Q82n48 streptomyc
1129	75.5	5.4	308	2	Q6QW75	Q6qw75 azospirillum
1130	75.5	5.4	312	2	Q9L449	Q9l449 azospirillum
1131	75.5	5.4	314	2	Q8FBD1	Q8fbd1 escherichia
1132	75.5	5.4	321	2	Q6FYD5	Q6fyd5 bartonella
1133	75.5	5.4	322	2	Q8UCR8	Q8ucr8 agrobacteri
1134	75.5	5.4	323	2	Q6GQ05	Q6gq05 xenopus lae
1135	75.5	5.4	324	2	Q9GEH5	Q9geh5 monochaetum
1136	75.5	5.4	328	2	Q9KDX8	Q9kdx8 bacillus ha
1137	75.5	5.4	343	2	Q6FUK1	Q6fuk1 candida gla
1138	75.5	5.4	352	2	Q71S48	Q71s48 ophiopholis
1139	75.5	5.4	353	2	Q99380	Q99380 chorda filu
1140	75.5	5.4	359	2	Q7BG29	Q7vg29 helicobacter
1141	75.5	5.4	364	2	Q6MB12	Q6mb12 parachlamyd
1142	75.5	5.4	368	2	Q85GC4	Q85gc4 abelia chin
1143	75.5	5.4	370	2	Q6D6F2	Q6d6f2 erwinia car
1144	75.5	5.4	379	2	Q6WRG7	Q6wrg7 bolomys tem
1145	75.5	5.4	383	2	Q7QT54	Q7qts4 giardia lam
1146	75.5	5.4	387	2	Q6FBC4	Q6fbc4 acinetobact
1147	75.5	5.4	388	2	Q6ML49	Q6ml49 dellolovibri
1148	75.5	5.4	396	2	Q7WTF8	Q7wtf8 streptomyc
1149	75.5	5.4	397	2	Q27976	Q27976 archaeoglob
1150	75.5	5.4	403	2	Q8RJL1	Q8rjl1 vibrio chol
1151	75.5	5.4	406	2	Q75D62	Q75d62 ashbya goss
1152	75.5	5.4	409	2	Q6PNA8	Q6pna8 steinernema
1153	75.5	5.4	419	2	Q734V3	Q734v3 bacillus ce
1154	75.5	5.4	425	2	Q9BK21	Q9bk21 caenorhabdi
1155	75.5	5.4	432	1	RPBX_SALTY	Q99191 salmonella
1156	75.5	5.4	439	2	Q8S3C1	Q8s3c1 thraustochy
1157	75.5	5.4	441	2	Q59179	Q59179 pyrococcus
1158	75.5	5.4	445	2	Q81S42	Q81s42 bacillus an
1159	75.5	5.4	452	1	YEER_ECOLI	P33016 escherichia
1160	75.5	5.4	452	2	Q6SLZ3	Q6slz3 bacillus li
1161	75.5	5.4	454	2	Q8XJ1	Q8xj1 shigella fl
1162	75.5	5.4	454	2	Q8XJ1	Q8xfj1 salmonella
1163	75.5	5.4	454	2	Q7CQB1	Q7cqb1 salmonella
1164	75.5	5.4	454	2	Q8FG56	Q8fg56 escherichia
1165	75.5	5.4	457	2	Q8FHA4	Q8fha4 escherichia
1166	75.5	5.4	459	1	TCR_STAAT	P02983 staphylococ
1167	75.5	5.4	459	1	TCR_STABP	P62967 staphylococ
1168	75.5	5.4	470	2	Q9KJVI	Q9kjni lactobacill
1169	75.5	5.4	476	1	MELB_SALTY	P30878 salmonella
1170	75.5	5.4	480	2	Q6APZ6	Q6apz6 desulfotale
1171	75.5	5.4	492	2	Q8Z5H6	Q8z5h6 salmonella
1172	75.5	5.4	492	2	Q9F798	Q9f798 salmonella
1173	75.5	5.4	494	2	Q67NV0	Q67nv0 symbiobacte
1174	75.5	5.4	498	2	Q9ZHR7	Q9zhr7 azospirillu
1175	75.5	5.4	499	2	Q8ZM30	Q8zm30 salmonella
1176	75.5	5.4	510	2	Q6GPD3	Q6gpd3 xenopus lae
1177	75.5	5.4	513	1	MEMP_ALCEU	Q07252 alcaigenes
1178	75.5	5.4	514	2	Q7N8B5	Q7n8b5 photorhabdu
1179	75.5	5.4	518	2	Q74283	Q74283 coprinus ci
1180	75.5	5.4	519	2	Q9FCP1	Q9fcp1 rhizobium l
1181	75.5	5.4	531	2	Q8EZV0	Q8ezv0 leptospira
1182	75.5	5.4	532	2	Q30727	Q30727 rhodobacter
1183	75.5	5.4	532	2	Q930J1	Q930j1 rhizobium m
1184	75.5	5.4	536	2	Q8SUS1	Q8sus1 encephalito
1185	75.5	5.4	540	2	Q6SG56	Q6sg56 bacillus li
1186	75.5	5.4	567	1	DSBD_CAMJE	Q9phr3 campylobact
1187	75.5	5.4	571	2	Q7MJ9	Q7mj9 vibrio vuln
1188	75.5	5.4	607	2	Q8SE1	Q8se1 trichosurus
1189	75.5	5.4	632	2	Q6BXV6	Q6bxv6 debaryomyce
1190	75.5	5.4	638	2	Q8ILF4	Q8ilf4 bacillus an
1191	75.5	5.4	646	2	Q6SD41	Q6sd41 bacillus li
1192	75.5	5.4	652	2	Q8WH42	Q8wh42 leptaulus c
1193	75.5	5.4	655	2	Q7NC25	Q7nc25 mycoplasma
1194	75.5	5.4	671	2	Q9TJU2	Q9tju2 danais xant
1195	75.5	5.4	672	2	Q8HUS4	Q8hus4 Jaimehinton
1196	75.5	5.4	676	1	CCMF_RHIME	P45404 rhizobium c
1197	75.5	5.4	679	2	Q8WGU3	Q8wgu3 pennantia c
1198	75.5	5.4	696	2	Q9THQ0	Q9thq0 emmenanthe
1199	75.5	5.4	696	2	Q9TIW3	Q9tiw3 romanzoffia

Q9tiw6 phacelia pa	696	2	Q9TIW6	Q9tiw6 phacelia pa
Q9tiy4 phacelia bo	696	2	Q9TIY4	Q9tiy4 phacelia bo
Q8mg4 acanthocaly	698	2	Q8MG4	Q8mg4 acanthocaly
Q6ff58 acinetobact	699	2	Q6FF58	Q6ff58 acinetobact
Q8wh66 hebenstreti	703	2	Q8WH66	Q8wh66 hebenstreti
Q8wh98 dichisma c	703	2	Q8WH98	Q8wh98 dichisma c
Q8frn3 corynebacte	703	2	Q8FRN3	Q8frn3 corynebacte
Q8m981 polyosma cu	717	2	Q8M981	Q8m981 polyosma cu
Q9tj5 pseudomussa	725	2	Q9TJ55	Q9tj5 pseudomussa
Q9tj9 emmenoptery	732	2	Q9TJ99	Q9tj9 emmenoptery
Q9ska9 arabidopsis	732	2	Q9SKA9	Q9ska9 arabidopsis
Q8wgu0 polyosma cu	735	2	Q8WGU0	Q8wgu0 polyosma cu
Q71q44 hebenstreti	740	2	Q71Q44	Q71q44 hebenstreti
Q71q44 polyosma ca	741	2	Q71Q44	Q71q44 polyosma ca
Q9t145 syringa emo	746	2	Q9T145	Q9t145 syringa emo
Q26432 oryctolagus	832	1	NAH3_RABIT	Q26432 oryctolagus
Q28362 didelphis m	839	1	NAH3_DIDMA	Q28362 didelphis m
Q69y98 homo sapien	870	2	Q69Y98	Q69y98 homo sapien
P39793 bacillus su	914	1	PBPA_BACSU	P39793 bacillus su
Q01623 caenorhabdi	932	2	Q01623	Q01623 caenorhabdi
Q7m7p8 wolnelli s	935	2	Q7M7P8	Q7m7p8 wolnelli s
Q7sev7 neurospora	995	2	Q7SEV7	Q7sev7 neurospora
Q52978 rhizobium m	999	1	PHAB_RHIME	Q52978 rhizobium m
Q8a203 bacteroides	1040	2	Q8A203	Q8a203 bacteroides
Q68441 agrobacteri	1046	2	Q68441	Q68441 agrobacteri
Q7q5q3 anopheles g	1094	2	Q7Q5Q3	Q7q5q3 anopheles g
Q651a5 oryza sativ	1471	2	Q651A5	Q651a5 oryza sativ
Q7r1f8 giardia lam	2180	2	Q7R1F8	Q7r1f8 giardia lam
Q8euk8 mycoplasma	121	2	Q8EUK8	Q8euk8 mycoplasma
Q6a5r2 propionibac	161	2	Q6A5R2	Q6a5r2 propionibac
Q6kde2 escherichia	193	2	Q6KDE2	Q6kde2 escherichia
Q8fj03 escherichia	194	2	Q8FJ03	Q8fj03 escherichia
Q7vdu9 prochloroco	208	2	Q7VDU9	Q7vdu9 prochloroco
Q96102 homo sapien	214	2	Q96102	Q96102 homo sapien
Q88fn8 pseudomonas	231	2	Q88FN8	Q88fn8 pseudomonas
Q81n55 bacillus an	240	2	Q81N55	Q81n55 bacillus an
Q7nbj4 mycoplasma	262	2	Q7NBJ4	Q7nbj4 mycoplasma
Q9kd01 bacillus ha	262	2	Q9KD01	Q9kd01 bacillus ha
Q7pba2 rickettsia	282	2	Q7PBA2	Q7pba2 rickettsia
Q8cta7 staphylococ	286	2	Q8CTA7	Q8cta7 staphylococ
Q04409 phaseolus v	289	2	Q04409	Q04409 phaseolus v
Q8zkt5 salmonella	290	1	REN_SALTY	Q8zkt5 salmonella
P93435 oryza sativ	291	2	P93435	P93435 oryza sativ
P14182 haemophilus	292	1	LICB_HAEIN	P14182 haemophilus
Q7yfa3 neimaymex	295	2	Q7YF33	Q7yfa3 neimaymex
Q7yft0 eciton burc	295	2	Q7YFT0	Q7yft0 eciton burc
Q7yft4 eciton mexi	295	2	Q7YFT4	Q7yft4 eciton mexi
Q55473 synechocyst	298	2	Q55473	Q55473 synechocyst
Q7p2a8 fusobacteri	299	2	Q7P2A8	Q7p2a8 fusobacteri
Q8u0a1 pyrococcus	302	2	Q8U0A1	Q8u0a1 pyrococcus
Q7vdf3 prochloroco	316	2	Q7VDF3	Q7vdf3 prochloroco
Q85j72 varanus sal	321	2	Q85J72	Q85j72 varanus sal
Q8u7a7 agrobacteri	322	2	Q8U7A7	Q8u7a7 agrobacteri
Q8jlr6 saccharomyc	339	2	Q8JLR6	Q8jlr6 saccharomyc
Q739k7 bacillus ce	360	2	Q739K7	Q739k7 bacillus ce
Q715y4 baionys tay	381	2	Q715Y4	Q715y4 baionys tay
Q66a18 bipes trida	382	2	Q66A18	Q66a18 bipes trida
Q14649 homo sapien	394	1	CIW3_HUMAN	Q14649 homo sapien
P75160 m putative	395	1	CDSA_MYCPN	P75160 m putative
Q59482 pyrococcus	398	2	Q59482	Q59482 pyrococcus
Q8rmj9 corynebacte	398	2	Q8RMJ9	Q8rmj9 corynebacte
Q8rjk4 vibrio chol	403	2	Q8RJK4	Q8rjk4 vibrio chol
Q01255 staphylococ	429	1	ARSB_STASY	Q01255 staphylococ
Q65u06 mannelmia	430	2	Q65U06	Q65u06 mannelmia
Q58733 pyrococcus	432	2	Q58733	Q58733 pyrococcus
Q6L0Y3	442	2	Q6L0Y3	Q6L0Y3
Q980K3 sulfobolus	451	2	Q980K3	Q980K3 sulfobolus
Q9vi79 drosophila	452	2	Q9VI79	Q9vi79 drosophila
Q8rtv1 uncultured	452	2	Q8RTV1	Q8rtv1 uncultured
Q94w70 buteo bureo	459	2	Q94WR0	Q94w70 buteo bureo
Q7szw7 brachydanio	459	2	Q7SZW7	Q7szw7 brachydanio
Q8vmx0 listeria mo	461	2	Q8VMX0	Q8vmx0 listeria mo

1273	75	5.4	461	2	Q8Y808	O8y8g8 listeria mo	1346	74.5	5.4	215	2	Q8XKC6	O8xkc6 clostridium
1274	75	5.4	473	1	YIHO_SALTY	O9l7r4 salmonella	1347	74.5	5.4	235	2	Q8ZQP8	Q8zqp8 salmonella
1275	75	5.4	478	2	Q7ZVQ2	O7vby0 strongyloce	1348	74.5	5.4	246	2	Q7VBY0	Q7vby0 strongyloce
1276	75	5.4	480	2	Q6QY99	O6qtr9 trypanosoma	1349	74.5	5.4	255	2	Q7IAR6	Q7iar6 psilodera a
1277	75	5.4	494	2	Q87S84	O87s84 vibrio para	1350	74.5	5.4	261	2	Q8EAF3	Q8eaf3 shewanella
1278	75	5.4	494	2	Q87S84	O87s84 vibrio chol	1351	74.5	5.4	265	2	Q8DFQ3	Q8dfq3 vibrio vuln
1279	75	5.4	495	2	Q7ML56	O7ml56 vibrio vuln	1352	74.5	5.4	268	2	Q8NSY4	Q8nsy4 corynebacte
1280	75	5.4	497	2	Q7U357	O7u357 bordetella	1353	74.5	5.4	271	2	Q7M8Y3	Q7m8y3 wolinnella s
1281	75	5.4	502	2	Q93226	O93226 arabidopsis	1354	74.5	5.4	273	2	Q6SGH5	Q6sgH5 uncultured
1282	75	5.4	507	2	Q92850	O92850 listeria in	1355	74.5	5.4	275	2	Q7MMN1	Q7mmn1 vibrio vuln
1283	75	5.4	522	1	NFF2_HUMAN	O9y5x5 homo sapien	1356	74.5	5.4	288	2	O23771	O23771 craterostig
1284	75	5.4	528	2	Q6CME2	O6cme2 kluyveromyc	1357	74.5	5.4	288	2	Q8BZP2	Q8bzp2 mus musculus
1285	75	5.4	528	2	Q7ZMR4	O7zmr4 kluyveromyc	1358	74.5	5.4	293	2	Q8U855	Q8u855 agrobacteri
1286	75	5.4	540	2	Q7XA06	O7xa06 arabidopsis	1359	74.5	5.4	297	2	Q9G226	Q9g226 rana sylvat
1287	75	5.4	540	2	Q6X1N2	O6xln2 bartonella	1360	74.5	5.4	301	2	O88169	O88169 enterococc
1288	75	5.4	544	2	Q7RG44	O7rg44 plasmodium	1361	74.5	5.4	302	2	Q832M6	Q832m6 enterococc
1289	75	5.4	546	2	Q65NCO	O65nc0 bacillus li	1362	74.5	5.4	304	2	Q8SKM6	Q8skm6 nitellopsis
1290	75	5.4	547	2	O8FTZ4	O8ftz4 corynebacte	1363	74.5	5.4	304	2	Q8SKM7	Q8skm7 lychnochamn
1291	75	5.4	551	1	FVR2_MOUSE	O9lxs5 mus musculu	1364	74.5	5.4	304	2	Q8SKM8	Q8skm8 lamprothamn
1292	75	5.4	569	2	Q6XJN3	O6xjn3 diploknema	1365	74.5	5.4	304	2	Q8SKM9	Q8skm9 chara conni
1293	75	5.4	570	2	Q6XJL4	O6xjl4 minusops co	1366	74.5	5.4	307	2	Q88EZ3	Q88ez3 pseudomonas
1294	75	5.4	573	2	Q6XJM5	O6xjm5 labramia co	1367	74.5	5.4	311	2	O51622	O51622 borrelia bu
1295	75	5.4	573	2	Q7VMZ4	O7vmz4 haemophilus	1368	74.5	5.4	313	2	Q860H0	Q860h0 homo sapien
1296	75	5.4	573	2	Q8XEY3	O8xey3 leptospira	1369	74.5	5.4	316	2	O7F2T9	O7f2t9 fusobacteri
1297	75	5.4	576	2	Q6XJH2	O6xjh2 tieghemella	1370	74.5	5.4	323	2	O16197	O16197 caenorhabdi
1298	75	5.4	580	2	Q6XJP8	O6xjp8 autranella	1371	74.5	5.4	324	1	MRAY_BACSU	Q03521 bacillus su
1299	75	5.4	580	2	Q85MB6	O85mb6 monoblephar	1372	74.5	5.4	324	2	Q8RXQ9	Q8rxq9 arabidopsis
1300	75	5.4	599	2	Q9LZD0	Q9lzd0 arabidopsis	1373	74.5	5.4	325	2	O9PAR1	O9par1 xylolla fas
1301	75	5.4	624	1	COX1_BACPF	Q04440 bacillus ps	1374	74.5	5.4	325	2	Q6ARZ8	Q6arz8 desulfotale
1302	75	5.4	643	2	O29273	O29273 archaeoglob	1375	74.5	5.4	341	2	Q6NYV2	Q6nyv2 brachydanio
1303	75	5.4	650	2	Q8WH99	Q8wh99 discophora	1376	74.5	5.4	359	2	Q6UJV6	Q6ujv6 timaspia ph
1304	75	5.4	650	2	Q6M029	O6mq29 bdellovibri	1377	74.5	5.4	361	2	Q8ZVM8	Q8zvm8 pyrobaculum
1305	75	5.4	656	2	Q6XJH1	O6xjh1 vitellariop	1378	74.5	5.4	362	2	Q8KB33	Q8kb33 chlomydia p
1306	75	5.4	658	2	Q6XJL3	O6xjl3 sideroxylyon	1379	74.5	5.4	366	2	O9Z6R4	O9z6r4 lamprothamn
1307	75	5.4	658	2	Q6XJK5	O6xjks payena luci	1380	74.5	5.4	367	2	O36050	O36050 lamprothamn
1308	75	5.4	658	2	Q6XJK8	O6xjk8 northea sey	1381	74.5	5.4	374	1	CIW9_HUMAN	Q9nnc2 homo sapien
1309	75	5.4	658	2	Q6XJL2	O6xjl2 minusops ze	1382	74.5	5.4	396	2	Q88HZ9	Q88hz9 pseudomonas
1310	75	5.4	658	2	Q6XJL3	O6xjl3 minusops el	1383	74.5	5.4	398	2	Q6A8D3	Q6aad3 propionibac
1311	75	5.4	658	2	Q6XJM4	O6xjm4 labramia ma	1384	74.5	5.4	399	2	O23485	O23485 caenorhabdi
1312	75	5.4	658	2	Q6XJM7	O6xjm7 faucherea p	1385	74.5	5.4	400	2	Q688H5	Q688h5 oryza sativ
1313	75	5.4	665	2	Q7Q4E5	Q7q4e5 anopheles g	1386	74.5	5.4	405	2	Q924N0	Q924n0 mus musculu
1314	75	5.4	685	2	Q6C7G7	O6c7g7 yarrowia li	1387	74.5	5.4	409	2	O06481	O06481 bacillus su
1315	75	5.4	693	2	Q31905	Q31905 borago offi	1388	74.5	5.4	410	2	Q6E8A0	Q6e8a0 erechttia sp
1316	75	5.4	696	2	Q9TIV0	O9tivo phacelia mi	1389	74.5	5.4	411	2	P93390	P93390 nicotiana t
1317	75	5.4	696	2	Q9TIV3	O9tiv3 nama serice	1390	74.5	5.4	414	2	Q638U4	Q638u4 bacillus ce
1318	75	5.4	699	2	Q9MUI9	Q9mui9 martynia an	1391	74.5	5.4	415	2	O94YV9	O94yv9 timmia bava
1319	75	5.4	702	2	Q8WHC4	O8whc4 solanum dip	1392	74.5	5.4	417	2	Q7YH69	Q7yh69 taenia asia
1320	75	5.4	705	2	Q6AP92	O6ap92 desulfotale	1393	74.5	5.4	419	2	Q8R0P1	Q8rop1 mus musculu
1321	75	5.4	743	2	Q9TLB0	O9tlb0 nematanthus	1394	74.5	5.4	424	2	Q6F9T4	Q6f9t4 acinetobact
1322	75	5.4	754	2	Q7KWK4	O7kwk4 dictyosteli	1395	74.5	5.4	426	2	Q6W2H2	Q6w2h2 rhizobium s
1323	75	5.4	820	2	Q9N429	Q9n429 caenorhabdi	1396	74.5	5.4	430	2	Q7TNE9	Q7tne9 mus musculu
1324	75	5.4	881	2	Q6FE07	Q6fe07 acinetobact	1397	74.5	5.4	430	2	Q9JK46	Q9jk46 mus musculu
1325	75	5.4	917	1	IL6B_MOUSE	Q00560 mus musculu	1398	74.5	5.4	439	2	Q66DX3	Q66dx3 yersinia ps
1326	75	5.4	917	2	Q6PDI9	O6pdi9 mus musculu	1399	74.5	5.4	439	2	Q8ZC24	Q8zcz4 yersinia ps
1327	75	5.4	939	2	Q669T0	O669t0 yersinia ps	1400	74.5	5.4	441	2	Q82E0E	Q82e0e bacillus an
1328	75	5.4	1012	2	Q95YI6	O95yi6 asterina pe	1401	74.5	5.4	441	2	Q6HFW1	Q6hfw1 bacillus th
1329	75	5.4	1047	2	Q7PNG3	O7png3 anopheles g	1402	74.5	5.4	447	2	Q17837	Q17837 caenorhabdi
1330	75	5.4	1056	2	O22855	O22855 arabidopsis	1403	74.5	5.4	450	2	O27920	O27920 bradyeia by
1331	75	5.4	1065	2	Q8A6B8	Q8a6b8 bacteroides	1404	74.5	5.4	451	2	Q8MPG6	Q8mpg6 trypanosoma
1332	75	5.4	1115	2	Q7QSA8	O7qsa8 giardia lam	1405	74.5	5.4	451	2	Q8K2E0	Q8k2e0 mus musculu
1333	75	5.4	1276	2	Q8MI49	Q8mi49 felis silve	1406	74.5	5.4	453	2	Q65DH6	Q65dh6 bacillus li
1334	75	5.4	1276	2	Q8MKD8	Q8mkd8 felis silve	1407	74.5	5.4	453	2	Q6LN43	Q6ln43 photobacter
1335	75	5.4	1280	2	Q95YI7	O95yi7 asterina pe	1408	74.5	5.4	453	2	Q6CVX8	Q6cvx8 erwinia car
1336	75	5.4	1294	1	YOH5_YEAST	Q08234 saccharomyc	1409	74.5	5.4	454	2	Q83W84	Q83w84 escherichia
1337	75	5.4	1612	2	Q6PYX7	O6pyx7 ostreococcu	1410	74.5	5.4	458	2	Q8CQF9	Q8cgf9 staphylococ
1338	75	5.4	1986	2	Q9IUJ3	O9iuj3 aconitum la	1411	74.5	5.4	469	1	MELE_ECOLI	F02921 escherichia
1339	75	5.4	2183	2	Q6W9E8	Q6w9e8 human echov	1412	74.5	5.4	469	2	Q7UBB0	Q7ubb0 shigella fl
1340	74.5	5.4	128	2	Q631X7	Q631x7 bacillus ce	1413	74.5	5.4	469	2	Q8XDU0	Q8xd00 escherichia
1341	74.5	5.4	141	2	Q9Z0Y8	O9zy08 arabidopsis	1414	74.5	5.4	471	2	Q81I29	Q81i29 bacillus ce
1342	74.5	5.4	174	2	Q97U88	Q97u88 sulfobus	1415	74.5	5.4	472	2	O66L46	O66l46 mus musculu
1343	74.5	5.4	184	2	Q68J88	Q68j88 gopherus po	1416	74.5	5.4	476	2	Q8Z9R4	Q8z9r4 salmonella
1344	74.5	5.4	201	2	Q8K6L8	Q8k6l8 streptococ	1417	74.5	5.4	476	2	Q8ZS16	Q8zsl6 salmonella
1345	74.5	5.4	202	2	Q7PHK7	O7phk7 anopheles g	1418	74.5	5.4	480	2	Q65GD6	Q65gd6 bacillus li

1419	74.5	5.4	481	2	Q83PA7	Q83pa7 shigella fl
1420	74.5	5.4	482	2	Q93QW4	Q93qw4 bacteroides
1421	74.5	5.4	483	2	Q85M60	Q85mf0 sallia bois
1422	74.5	5.4	488	2	Q8FA73	Q8fa73 acineobact
1423	74.5	5.4	492	2	Q67LL3	Q67ll3 symbiobacte
1424	74.5	5.4	503	2	Q66IG1	Q66ig1 xenopus tro
1425	74.5	5.4	507	2	Q83W34	Q83w34 rickettsia
1426	74.5	5.4	529	1	G161_HUMAN	Q8n6u8 homo sapien
1427	74.5	5.4	533	2	Q8K376	Q8k376 mus musculu
1428	74.5	5.4	535	2	Q84KR3	Q84kr3 oryza sativ
1429	74.5	5.4	535	2	Q69JW3	Q69jw3 oryza sativ
1430	74.5	5.4	544	2	Q44965	Q44965 caenorhabdi
1431	74.5	5.4	547	2	Q73WU9	Q73wu9 mycobacteri
1432	74.5	5.4	560	2	Q44703	Q44703 caenorhabdi
1433	74.5	5.4	564	2	Q6H9P4	Q6h9f4 monttea chi
1434	74.5	5.4	567	2	Q8BGX8	Q8bgx8 m mus muscu
1435	74.5	5.4	580	2	Q63EP4	Q63ep4 bacillus ce
1436	74.5	5.4	588	2	Q7XPE1	Q7xpe1 oryza sativ
1437	74.5	5.4	589	2	Q8X120	Q8x120 exophiala d
1438	74.5	5.4	592	2	Q8BUR1	Q8bur1 mus musculu
1439	74.5	5.4	594	2	Q8GEW2	Q8gew2 coris monsp
1440	74.5	5.4	600	2	Q8EVN3	Q8evn3 lamprotham
1441	74.5	5.4	606	2	Q86LGO	Q86lgo drosophila
1442	74.5	5.4	610	2	Q70SP5	Q70sp5 limosella g
1443	74.5	5.4	612	2	Q76FH0	Q76fh0 auxis roche
1444	74.5	5.4	612	2	Q76G39	Q76g39 auxis roche
1445	74.5	5.4	612	2	Q8HKX9	Q8hkx9 pterocasio
1446	74.5	5.4	616	2	Q7QWH6	Q7qwh6 giardia lam
1447	74.5	5.4	631	2	Q8THX4	Q8thx4 methanosarc
1448	74.5	5.4	633	1	PAIRE_MYCGA	Q59526 mycoplasma
1449	74.5	5.4	635	2	Q89H46	Q89496 coliphage nit
1450	74.5	5.4	645	2	Q8WH87	Q8wh87 emmoltum nit
1451	74.5	5.4	647	2	Q8GEW3	Q8gew3 clavia eue
1452	74.5	5.4	663	2	Q84799	Q84799 escalonia
1453	74.5	5.4	675	2	Q7YAM5	Q7yam5 chara vulga
1454	74.5	5.4	684	2	Q9TK71	Q9tk71 montia diff
1455	74.5	5.4	688	2	Q7YML2	Q7ym12 brunfelsia
1456	74.5	5.4	690	2	Q9TIW4	Q9tiw4 hesperochir
1457	74.5	5.4	695	2	Q8MJV2	Q8mjv2 merxmuelle
1458	74.5	5.4	695	2	Q9TI18	Q9tit8 eucrypta ch
1459	74.5	5.4	697	2	Q9HTI2	Q9htit2 phacelia ra
1460	74.5	5.4	697	2	Q8HTZ3	Q8htz3 anthocercis
1461	74.5	5.4	700	2	Q9TLG0	Q9tlg0 amphianthus
1462	74.5	5.4	701	2	Q8MVL7	Q8mvl7 abutilon hy
1463	74.5	5.4	705	2	Q8E571	Q8e571 aureolaria
1464	74.5	5.4	714	2	Q9TK85	Q9tk85 aluauadia h
1465	74.5	5.4	726	2	Q19937	Q19937 emorya suav
1466	74.5	5.4	740	2	Q9MTR0	Q9mtr0 quintinia v
1467	74.5	5.4	741	2	Q71QJ8	Q71qu8 tridax balb
1468	74.5	5.4	741	2	Q85Z03	Q85z03 stevia reba
1469	74.5	5.4	744	2	Q9MTR4	Q9mtr4 nephrophyll
1470	74.5	5.4	794	1	X366_CORGL	P35867 corynebacte
1471	74.5	5.4	799	2	Q75G84	Q75g84 oryza sativ
1472	74.5	5.4	804	2	Q7NLY9	Q7nly9 gloeobacter
1473	74.5	5.4	869	1	MUTS_THETN	Q8ra71 thermoanaer
1474	74.5	5.4	889	2	Q8YS17	Q8ysl7 anabaena sp
1475	74.5	5.4	1118	2	Q85U88	Q85u88 mantheimia
1476	74.5	5.4	1124	2	Q86UF3	Q86uf3 homo sapien
1477	74.5	5.4	1132	2	Q7QZ72	Q7qz72 giardia lam
1478	74.5	5.4	1449	2	Q6AXE3	Q6axe3 mus musculu
1479	74.5	5.4	121	2	Q8W533	Q8w533 setaria ita
1480	74	5.3	212	2	Q6TGU5	Q6tg05 brachydanio
1481	74	5.3	212	2	Q7ZUB3	Q7zub3 brachydanio
1482	74	5.3	217	2	P70017	P70017 xenopus lae
1483	74	5.3	231	2	Q89265	Q89265 gallid herp
1484	74	5.3	231	2	Q782M9	Q782m9 gallid herp
1485	74	5.3	238	2	Q75204	Q75204 homo sapien
1486	74	5.3	238	2	Q8BG95	Q8bgp5 m mus muscu
1487	74	5.3	242	2	Q48598	Q48598 lactococcus
1488	74	5.3	268	2	Q7YTL8	Q7ytl8 caenorhabdi
1489	74	5.3	271	2	Q94VC8	Q94vc8 varanus pil
1490	74	5.3	277	2	Q9Z779	Q9z779 chlamydia p
1491	74	5.3	281	2	Q97WM7	Q97wm7 sulfolobus
1492	74	5.3	295	2	Q7YFS7	Q7yfs7 nomamymex
1493	74	5.3	295	2	Q6CVN2	Q6cyn2 erwinia car
1494	74	5.3	295	2	Q7ZY07	Q7zy07 xenopus lae
1495	74	5.3	296	1	GLTR_BACSU	P94501 bacillus su
1496	74	5.3	300	2	Q6G458	Q6g458 bartonella
1497	74	5.3	303	2	O01459	O01459 caenorhabdi
1498	74	5.3	304	2	O01459	O01459 synechococc
1499	74	5.3	311	2	Q87M27	Q87m27 vibrio para
1500	74	5.3	321	2	Q94VA9	Q94va9 varanus sal

ALIGNMENTS

RESULT 1

Q6UX65	PRELIMINARY;	PRT;	266 AA.
ID	Q6UX65		
AC	Q6UX65;		
DT	05-JUL-2004 (TReMBLrel. 27, Created)		
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)		
DE	WRFQ154.		
GN	ORFNames=UNQ154;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment."		
RL	Genome Res. 13:2265-2270(2003).		
DR	EMBL: AY358492; AAQ88856.1; -.		
SQ	SEQUENCE 266 AA; 29766 MW; 4F91D5C212D458E5 CRC64;		
Query Match 100.0%; Score 1392; DB 2; Length 266;			
Best Local Similarity 100.0%; Pred. No. 1.2e-107;			
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MMWFQGLSLPSALVITWSAAFI	PSYITAVTLHHIDPALPYISDTGTVAPEKLCFGAML 60
Db	1	MMWFQGLSLPSALVITWSAAFI	PSYITAVTLHHIDPALPYISDTGTVAPEKLCFGAML 60
Qy	61	NIAAVLCIATIIYRYKQVHALSPEENVII	IKLNKAGVLGILSCGLSIVANFQKTLFAA 120
Db	61	NIAAVLCIATIIYRYKQVHALSPEENVII	IKLNKAGVLGILSCGLSIVANFQKTLFAA 120
Qy	121	HVSGAVLTFGMSLYMFVQTILSYQMPKIHGQVFWIRLLLVICGVSALSMTCSSVL 180	
Db	121	HVSGAVLTFGMSLYMFVQTILSYQMPKIHGQVFWIRLLLVICGVSALSMTCSSVL 180	
Qy	181	HSGNFGTDLEOKLHWPEDKGYVLHMTTAAEWSMSPFSGFFLTIRDFQKLSLRVEAN 240	
Db	181	HSGNFGTDLEOKLHWPEDKGYVLHMTTAAEWSMSPFSGFFLTIRDFQKLSLRVEAN 240	
Qy	241	LHGTLTYDTAPCPINNERTLLSRDI 266	
Db	241	LHGTLTYDTAPCPINNERTLLSRDI 266	

RESULT 2

Q9CR48

IO Q9CR48 PRELIMINARY; PRT; 267 AA.
AC Q9CR48;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610318G18 product:hypothetical protein, full
DE insert sequence (Mus musculus adult male tongue cDNA, RIKEN full-
DE length enriched library, clone:2310056E801 product:hypothetical
DE protein, full insert sequence) (Mus musculus 10 days lactation, adult
DE female mammary gland cDNA, RIKEN full-length enriched library,
DE clone:D730039I03 product:hypothetical protein, full insert
DE sequence)
GN Name=2610318G18Rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs".
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue, and Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK012044; BAB27990.1; -;
DR EMBL; AK009940; BAB26598.1; -;
DR EMBL; AK052824; BAC35162.1; -;
DR MGD; MGI:1914421; 2610318G18Rik.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 30227 MW; 228214D5AFF36783 CRC64;

Query Match 89.4%; Score 1245; DB 2; Length 267;
Best Local Similarity 86.4%; Pred. No.2e-95;
Matches 229; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MWFFQGLSFLPSALVWTSAAFIPIFYITPAVTLHHIDPALPIYISDTGTVAPEKCLFGAML 60
DB 1 MWFFQGLSFLPSALVWTSAAFIPIFYITPAVTLHHIDPALPIYISDTGTVAPEKCLFGAML 60

QY 61 NTAAVLCIATYVRYKQVHALSPENVIKLNKAGLVGLISCLGLSIVANFQKTLFLAA 120
DB 61 NTAAVLCIATYVRYKQVHALSPENVIKLNKAGLVGLISCLGLSIVANFQKTLFLAA 120

QY 121 HVSGLVITFGMSGLYMFVQTILSYQMPKIHGKQVFIWLLVIVCGVSALSMLTCSVL 180
DB 121 HVSGLVITFGMSGLYMFVQTILSYQMPKIHGKQVFIWLLVIVCGVSALSMLTCSVL 180

QY 181 HSGNFGTDEQKLHWNPKDGYLVLMHTTAAWSMSFSFGFFLTYYRDFQKISLRVAN 240
DB 181 HSGNFGTDEQKLHWNPKDGYLVLMHTTAAWSMSFSFGFFLTYYRDFQKISLRVAN 240

QY 241 LHGLTLTYDTAPCPINNETRLLSRD 265
DB 241 LHGLTLTYDTAPCPINNETRLLSRD 265

RESULT 3
Q9D520 PRELIMINARY; PRT; 267 AA.
ID Q9D520;
AC Q9D520;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4930524M19 product:hypothetical protein, full insert
DE sequence.
GN Name=2610318G18Rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";

GN ORNames=zgc:86754;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=23389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071426; AAH71426.1; -;
DR ZFIN; ZDB-GENE-040625-141; zgc:86754.
SQ SEQUENCE 272 AA; 30362 MW; B7FE8BDD89FC87FA CRC64;

Query Match 54.9%; Score 764.5; DB 2; Length 272;
Best Local Similarity 55.2%; Pred. No. 1.7e-55;
Matches 138; Conservative 48; Mismatches 63; Indels 1; Gaps 1;

Qy 1 MWFFQGLSPALSVIWTSAATFYSITATVTLHHIDPALPIYDGTGVAPEKCLFGAML 60
Db 1 MWFFQGLCVLPVALVWMTATTFATFATVAVLRHVDLPVYISDGTGVAPEKCVFGWML 60

Qy 61 NIAAVLCIATYVRYKQVHALSP-EENVIIKLNKAGLVGLSLGILSIVANFQKTLTFA 119
Db 61 NVSAFLGVATVYRYKQLQALADVDDTRLNLNVGVFVFGCCSFGMCVWVFQKTLTFS 120

Qy 120 AHVSGAVLTFGMSLYMFVQILSYQMPKIHGQVFWIRLLVWCVSLSMLTCSV 179
Db 121 MHLVGAILTFGIGALYFVQIALSYLQMPHITKMTFTRLSVGIWTLSSITSMFVSVI 180

Qy 180 LHSGNFGTDLQKLHWPEDKGYVLMITTAASMSMSPFPGFFLTIRDFQKISLRVEANLGLTYDTA 239
Db 181 MISTLPGVGVNKKLHWTFEGEFTAHIVSTISEWSLSLSFISFPLTYIRDFPKINLRASA 240

Qy 240 NLHGLTYDT 249
Db 241 ELQSNHLYES 250

RESULT 7
Q8NBQ4
ID AC Q8NBQ4 PRELIMINARY; PRT; 136 AA.
RC TISSUE=Liver;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE InterPro; IPR000504; RNA_rec_mot.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075350; BAC11562.1; -;
SQ SEQUENCE 136 AA; 15728 MW; 984FEDC29636ACOC CRC64;

Query Match 52.1%; Score 725; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.7e-52;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 MGSLYMFVQILSYQMPKIHGQVFWIRLLVWCVSLSMLTCSVLHSGNFGTDLT 190
Db 1 MGSLYMFVQILSYQMPKIHGQVFWIRLLVWCVSLSMLTCSVLHSGNFGTDLT 60

Qy 191 QKLHWPEDKGYVLMITTAASMSMSPFPGFFLTIRDFQKISLRVEANLGLTYDTA 250
Db 61 QKLHWPEDKGYVLMITTAASMSMSPFPGFFLTIRDFQKISLRVEANLGLTYDTA 120

Qy 251 PCPINNERTLLSRDI 266
Db 121 PCPINNERTLLSRDI 136

RESULT 8
Q8N682
ID Q8N682 PRELIMINARY; PRT; 238 AA.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018435; AAH18435.1; -;
DR InterPro; IPR000504; RNA_rec_mot.
DR InterPro; IPR009058; Wing_hlx_bnd.

Best Local Similarity 35.8%; Pred. No. 3.1e-24;
Matches 83; Conservative 49; Mismatches 93; Indels 7; Gaps 2;

QY 8 LSELPALVITWTSAAFTSYTAVTLHHIDPALPYISDTCTVAPEKCLFGAMLNIAAVLC 67
DB 25 LYLPLISVFLNFPTFTGTTIAAQLQHVVTPTVYISDAATYSPSCVCFQFQINIGCVLL 84
QY 68 IATIVYKQVHAL----SPENVIIKLKAGLVILGILSGISIVANFOKTLFAAHVS 123
DB 85 GTIIVYRQIQELSPRHSVDRQALGRCSGIGFWIGSGISIVGNFOETNVRIVHYV 144
QY 124 GAVLTFGMGLYFVQITLSPQKIHGQVFWIRLLVILVIGVSALSMCLTCSSVLHSG 183
DB 145 GAFSLFGLGTYVFIQSYISYIQPYMGTKQKANLWALSVCVTFPMIIVAVTVGISHL 204
QY 184 NFGTDLQKHLNPNEDKGYVLHMITTAAEWSMSFSFGFELTYRDPQKISL 235
DB 205 FRGTDPRK--WYPSDGGWYHVASSISEIVATAFCFYVLTFTDEBRTMQL 253

RESULT 13
077262
ID O77262 PRELIMINARY; PRT; 246 AA.
AC O77262;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CQ4025-PA (EG:22E5.9 protein) (UPI0820p).
GN Name=EG:22E5.9; ORFNames=CQ4025;
OS Drosophila melanogaster (Fruit fly).
GN Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Furi V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodrager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
RP MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirekas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
SEQUENCE FROM N.A.
RP MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirekas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
SEQUENCE FROM N.A.
RP MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBDJ databases.
[6]
SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBDJ databases.
[7]
SEQUENCE FROM N.A.
RP Murphy L., Harris D., Barrell B.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBDJ databases.
[8]
SEQUENCE FROM N.A.
RP Benos P.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBDJ databases.
[9]
SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Faragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AS003423; AAP45721.1; -;
DR EMBL; AL031765; CAA21131.1; -;
DR EMBL; AY118613; AAM49982.1; -;
DR FIR; T13747; T13747.
DR FlyBase; FBgn0025624; CG4025.
SQ SEQUENCE 246 AA; 27773 MW; 9E1C3EC764A644E4 CRC64;

Query Match 26.0%; Score 361.5; DB 2; Length 246;
Best Local Similarity 33.6%; Pred. No. 4.8e-22;
Matches 78; Conservative 50; Mismatches 91; Indels 13; Gaps 4;


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Qy 11 LPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIAT 70
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LPVLTFLIFQVTLGTYIFAVLEGHVPTVPIYISDAATYSPESCVCQOLINIGSVLLGIT 66

Qy 71 IYRYKQVHAL---SPE-ENVIIKLNKAGLVGLSCIGLSIVANFQKTLTFAAHVSGAV 126
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 IYRYRQVLQYLEHHPDLGSLRQRLALWFLVSLGIGISFVGNFQETNVRIVHFICAF 126

Qy 127 LTFGMSLYMVFQITLSYQMPKIHGKQVFWIRLLLVICGVSALSML---TCSSVLHSG 183
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 CFCGGLTYFWQALISYLIIFPMGSTRINAHRLRGMVSVCTILFILLAVTGVMSHILFKG 186

Qy 184 NFGTLEOKLHNPEDKGYVLHMITTAAEWSMSPSFFGFITYIRDFQKISL 235
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 -----QNPKWYSDGQWYHVVSSISEWVIATVFSFILLFTNEFRDVS 232

RESULT 14
ID Q86F93 PRELIMINARY; PRT; 252 AA.
AC Q86F93;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Clone Z2242 mRNA sequence.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA Wang S.Y., Fu G., Zhang X.B., Wang Z.Q., Brindley P.J., McManus D.P.,
RA Xue C.L., Feng Z., Chen Z., Han Z.G.;
RT "Evolutionary and biomedical implications of a Schistosoma japonicum
RT complementary DNA resource.";
RL Nat. Genet. 35:139-147(2003).
DR EMBL; AY222970; AAP05982.1; -.
SQ SEQUENCE 252 AA; 28444 MW; 64035F88B507B3F0 CRC64;

Query Match 22.9%; Score 318.5; DB 2; Length 252;
Best Local Similarity 29.6%; Pred. No. 1.8e-18;
Matches 79; Conservative 48; Mismatches 97; Indels 43; Gaps 9;

Qy 14 ALVITWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYV 73
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 AFIVAIVGTFICISYLISTSDNHASITLFPYISDTGALPEPESCIFGQLLNICSFLCFVCYC 71

Qy 74 RYKQVHALS-----PEENVIIKLNKAGLVGLSCIGLSIVANFQKTLTFAAHVSGAV 126
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 WY--LHSCSVIRARHGPYSHII--FSRVTCTVGCISLGMMSVANFQEASLIVVHLIGAI 127

Qy 127 LTFGMSLYMVFQITLSYQMPKIHGKQVFWIRLLLVICGVSALSMLTC 176
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 MTFNLGVIFAAALVTFSTRKHLDYNF-----RYIFAILITIFGLANVGVFIPLR-- 178

Qy 177 SSVLHSGNFGTDLRQKLHNPEDKGYVLHMITTAAEWSMSPSFFGFITYIRDFQKISLR 236
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 -----SGLSGPFPRK--WDPSEPGTYVHAMSFCEWLMSPFILFLFFFSMIFELKNVY-- 229

Qy 237 VEANLHGLTYDTPACPINNERTLLS 263
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 ----LHSVYKQVHYISTGNNEQTPLA 252
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RESULT 15

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Q93319
ID Q93319 PRELIMINARY; PRT; 271 AA.
AC Q93319;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
```

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein C33A11.2.
GN ORFNames=C33A11.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=99089613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Gajadaty S.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z79597; CAB01861.1; -.
DR PIR; T19654; T19654.7878; C33A11.2.
DR Wormbase; WBGene00007878; C33A11.2; CE08547.
DR WormPep; C33A11.2; CE08547.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 30993 MW; 2B715BAP872CCBC8 CRC64;

Query Match 20.7%; Score 288; DB 2; Length 271;
Best Local Similarity 30.9%; Pred. No. 6.8e-16;
Matches 71; Conservative 43; Mismatches 104; Indels 12; Gaps 6;

Qy 14 ALVITWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYV 73
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 ALIFFVQSFFV--YTTAVLKHDVDPFPYLLSSAADKRPQSCIFAIGANISSVLLALVVFV 75

Qy 74 RYKQVHALSP--EENVIIKLNKAGLVGLSCIGLSIVANFQKTLTFAAHVSGAVLTFGM 131
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 RYQLRGIPAPYDEANLQAWNWRQKWFYIALLGLFFVANVQETAIIPVHMSSAVASFGG 135

Qy 132 GSLYMVFQITLSYQMPKIHGKQVFWIRLLLVICGVSALSML-LTCSSVLHSGNFGT 187
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 FSIYMIFFQCYLTHRVPTTITLRTVYRVYRVTIFPSVICFCCSFGFGIAASKIFHKTY--P 193

Qy 188 DLQKHLWNDE--DKGYVLHMITTAAEWSMSPSFFGFITYIRDFQKISL 235
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 DLTPRPWRRYIQPGYELHQLSALAEWGCAISQIFPIQSFGPEFEDISL 243
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Search completed: August 26, 2005, 17:29:45

Job time : 227 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:50:35 ; Search time 43 Seconds
(without alignments)
461.783 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MWFFQGLSLPSALVIWTS.....YDTAPCPINNERTLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCFUS COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1388	99.7	267	4	US-09-663-600A-190
2	595.5	42.8	172	4	US-09-663-600A-96
3	479.5	34.4	238	3	US-09-724-864-38
4	358	25.7	69	4	US-09-663-600A-130
5	358	25.7	69	4	US-09-663-600A-224
6	118	8.5	21	3	US-08-905-223-20
7	118	8.5	21	3	US-09-247-155-20
8	118	8.5	21	4	US-09-663-600A-20
9	118	8.5	21	4	US-09-621-976-2
10	118	8.5	21	4	US-09-513-999C-2
11	118	8.5	21	4	US-09-471-276-2
12	91.5	6.6	291	4	US-09-107-532A-4147
13	91.5	6.6	387	4	US-09-721-870-14
14	90	6.5	283	4	US-09-602-787A-588
15	90	6.5	396	4	US-09-248-796A-20434
16	88	6.3	344	4	US-09-248-796A-16383
17	88	6.3	1165	1	US-08-240-357-2
18	86.5	6.2	356	4	US-09-134-000C-4914
19	85.5	6.1	579	4	US-09-786-681A-4
20	85.5	6.1	582	4	US-09-786-681A-2
21	85	6.1	419	4	US-09-948-774-2
22	85	6.1	1180	3	US-08-736-214-12
23	84.5	6.1	296	4	US-09-134-000C-6205
24	84	6.0	241	4	US-09-328-352-8001
25	84	6.0	506	4	US-09-540-236-2605
26	84	6.0	537	4	US-09-489-039A-14149
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103	76	5.5	424	4	US-09-252-991A-18895	Sequence 18895, A	176	73.5	5.3	693	1	US-09-252-991A-19167	Sequence 19167, A
104	76	5.5	429	4	US-09-522-501-10	Sequence 10, Appl	177	73.5	5.3	717	4	US-09-134-000C-5833	Sequence 5833, Ap
105	76	5.5	435	6	5268463-9	Patent No. 5268463	178	73.5	5.3	1099	3	US-08-726-214-14	Sequence 14, Appl
106	76	5.5	435	6	5268463-9	Patent No. 5268463	179	73.5	5.3	2020	1	US-07-551-531-2	Sequence 2, Appli
107	76	5.5	453	4	US-09-252-991A-17394	Sequence 17394, A	180	73.5	5.3	2485	5	PCT-US94-00198-1	Sequence 1, Appli
108	76	5.5	453	4	US-09-949-016-10337	Sequence 10337, A	181	73.5	5.3	2485	5	PCT-US94-00198-2	Sequence 2, Appli
109	75.5	5.4	633	4	US-09-352-991A-27163	Sequence 27163, A	182	73.5	5.3	2818	1	US-08-510-284-1	Sequence 1, Appli
110	75.5	5.4	401	4	US-09-489-039A-11546	Sequence 11546, A	183	73.5	5.3	2818	1	US-08-411-383-2	Sequence 2, Appli
111	75.5	5.4	445	4	US-09-328-352-6669	Sequence 6669, Ap	184	73.5	5.3	2818	3	US-08-449-933-2	Sequence 2, Appli
112	75.5	5.4	517	4	US-09-248-796A-20437	Sequence 20437, A	185	73.5	5.3	2818	3	US-07-966-049A-2	Sequence 2, Appli
113	75.5	5.4	1155	4	US-09-543-681A-6286	Sequence 6286, Ap	186	73.5	5.3	2818	3	US-09-542-331-2	Sequence 2, Appli
114	75.5	5.4	1172	4	US-09-328-352-6071	Sequence 6071, Ap	187	73.5	5.3	2818	3	US-09-510-791-2	Sequence 2, Appli
115	75	5.4	218	4	US-09-328-352-5215	Sequence 5215, Ap	188	73	5.2	178	4	US-09-328-352-5593	Sequence 5593, Ap
116	75	5.4	283	4	US-09-107-433-3024	Sequence 3024, Ap	189	73	5.2	187	4	US-09-328-352-7918	Sequence 7918, Ap
117	75	5.4	290	3	US-09-134-001C-4893	Sequence 4893, Ap	190	73	5.2	234	4	US-09-270-767-45527	Sequence 45527, A
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119	75	5.4	344	3	US-09-058-376-1	Sequence 1, Appli	192	73	5.2	431	4	US-09-710-279-2566	Sequence 2566, Ap
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121	75	5.4	399	4	US-09-489-039A-9414	Sequence 9414, Ap	194	73	5.2	445	2	US-08-900-148-2	Sequence 2, Appli
122	75	5.4	408	4	US-09-719-088B-2	Sequence 2, Appli	195	73	5.2	466	3	US-09-134-001C-3355	Sequence 3355, Ap
123	75	5.4	420	3	US-09-255-368-6	Sequence 6, Appli	196	73	5.2	727	4	US-09-815-923-10	Sequence 10, Appl
124	75	5.4	420	4	US-09-405-558-6	Sequence 6, Appli	197	73	5.2	3079	5	PCT-US94-00198-4	Sequence 4, Appli
125	75	5.4	457	4	US-09-489-039A-8037	Sequence 8037, Ap	198	72.5	5.2	227	4	US-09-583-110-3621	Sequence 3621, Ap
126	75	5.4	524	4	US-09-248-796A-20256	Sequence 20256, A	199	72.5	5.2	281	4	US-09-540-236-2349	Sequence 2349, Ap
127	75	5.4	579	4	US-09-720-317A-4	Sequence 4, Appli	200	72.5	5.2	319	4	US-09-543-681A-5398	Sequence 5398, Ap
128	74.5	5.4	304	4	US-09-328-352-6459	Sequence 6459, Ap	201	72.5	5.2	389	4	US-09-328-352-5055	Sequence 5055, Ap
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130	74.5	5.4	340	4	US-09-543-681A-5778	Sequence 5778, Ap	203	72.5	5.2	519	4	US-09-489-039A-13346	Sequence 13346, A
131	74.5	5.4	367	4	US-09-198-452A-1069	Sequence 1069, Ap	204	72.5	5.2	519	4	US-09-248-796A-20368	Sequence 20368, A
132	74.5	5.4	367	4	US-09-438-185A-996	Sequence 996, App	205	72.5	5.2	607	4	US-09-328-352-5096	Sequence 5096, Ap
133	74.5	5.4	384	4	US-09-248-796A-20119	Sequence 20119, A	206	72	5.2	261	4	US-09-538-092-318	Sequence 318, App
134	74.5	5.4	388	4	US-09-949-016-7631	Sequence 7631, Ap	207	72	5.2	273	4	US-09-328-352-5843	Sequence 5843, Ap
135	74.5	5.4	405	4	US-09-719-088B-3	Sequence 3, Appli	208	72	5.2	337	4	US-09-902-540-13005	Sequence 13005, A
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137	74.5	5.4	436	6	5432081-10	Patent No. 5432081	210	72	5.2	430	3	US-09-134-001C-2981	Sequence 2981, Ap
138	74.5	5.4	436	6	5432081-10	Patent No. 5432081	211	72	5.2	468	4	US-09-543-681A-4671	Sequence 4671, Ap
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140	74.5	5.4	475	4	US-09-248-796A-20067	Sequence 20067, Ap	213	72	5.2	502	4	US-09-579-250-12	Sequence 12, Appl
141	74.5	5.4	556	4	US-09-248-796A-20229	Sequence 20229, A	214	72	5.2	502	4	US-09-579-250-14	Sequence 14, Appl
142	74.5	5.4	601	1	US-08-194-338-2	Sequence 2, Appli	215	72	5.2	506	4	US-09-252-991A-25852	Sequence 25852, A
143	74.5	5.4	1798	4	US-09-270-767-60233	Sequence 60233, A	216	72	5.2	569	3	US-08-750-723A-2	Sequence 2, Appli
144	74.5	5.4	2410	4	US-09-270-767-44775	Sequence 44775, A	217	72	5.2	569	3	US-09-191-275-2	Sequence 2, Appli
145	74	5.3	173	4	US-09-252-991A-22033	Sequence 22033, A	218	72	5.2	906	1	US-08-190-802A-31	Sequence 31, Appl
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148	74	5.3	280	4	US-09-438-185A-829	Sequence 829, App	221	72	5.2	906	4	US-08-487-072A-31	Sequence 31, Appl
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151	74	5.3	292	3	US-09-348-116A-2	Sequence 2, Appli	224	71.5	5.1	237	3	US-09-115-934A-3	Sequence 3, Appli
152	74	5.3	332	4	US-09-902-540-15291	Sequence 15291, A	225	71.5	5.1	237	4	US-09-611-175-3	Sequence 3, Appli
153	74	5.3	445	4	US-08-937-834-5	Sequence 5, Appli	226	71.5	5.1	287	3	US-09-134-001C-5055	Sequence 5055, Ap
154	74	5.3	448	4	US-09-543-681A-7245	Sequence 7245, Ap	227	71.5	5.1	292	4	US-09-489-039A-12212	Sequence 12212, A
155	74	5.3	487	4	US-09-949-016-9649	Sequence 9649, Ap	228	71.5	5.1	372	3	US-08-501-003A-12	Sequence 12, Appl
156	74	5.3	727	4	US-09-543-681A-7968	Sequence 7968, Ap	229	71.5	5.1	379	3	US-09-740-035-4	Sequence 4, Appli
157	74	5.3	800	3	US-09-134-001C-5655	Sequence 5655, Ap	230	71.5	5.1	383	2	US-08-501-003A-14	Sequence 14, Appl
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159	73.5	5.3	360	1	US-08-597-236-11	Sequence 11, Appl	232	71.5	5.1	391	2	US-08-501-003A-13	Sequence 13, Appl
160	73.5	5.3	360	1	US-08-746-682A-11	Sequence 11, Appl	233	71.5	5.1	391	4	US-09-949-016-5904	Sequence 5904, Ap
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162	73.5	5.3	391	1	US-08-103-445-5	Sequence 5, Appli	235	71.5	5.1	411	4	US-09-949-016-8100	Sequence 8100, Ap
163	73.5	5.3	391	1	US-08-461-690B-5	Sequence 5, Appli	236	71.5	5.1	412	4	US-10-138-701-59	Sequence 59, Appl
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166	73.5	5.3	391	4	US-09-275-252A-13	Sequence 13, Appl	239	71.5	5.1	521	4	US-09-438-185A-523	Sequence 523, App
167	73.5	5.3	395	4	US-09-489-039A-12123	Sequence 12123, A	240	71.5	5.1	535	4	US-09-252-991A-21652	Sequence 21652, A
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171	73.5	5.3	428	4	US-09-438-185A-682	Sequence 682, App	244	71	5.1	201	4	US-09-270-767-33463	Sequence 33463, A
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249	71	5.1	388	4	US-09-222-938A-37	Sequence 37, Appl	322	70	5.0	594	4	US-09-489-039A-10622	Sequence 10622, A
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251	71	5.1	404	4	US-09-107-433-3747	Sequence 3747, Ap	324	70	5.0	708	1	US-07-797-556-2	Sequence 2, Appli
252	71	5.1	408	4	US-09-489-039A-9583	Sequence 9583, Ap	325	70	5.0	708	1	US-08-308-881-2	Sequence 2, Appli
253	71	5.1	454	4	US-09-489-847-305	Sequence 305, App	326	70	5.0	708	2	US-09-058-263-2	Sequence 2, Appli
254	71	5.1	461	4	US-09-043-944-1	Sequence 1, Appli	327	70	5.0	708	2	US-09-059-099-2	Sequence 2, Appli
255	71	5.1	465	4	US-09-043-944-6	Sequence 6, Appli	328	70	5.0	708	3	US-09-058-264-2	Sequence 2, Appli
256	71	5.1	465	4	US-09-710-279-1676	Sequence 1676, Ap	329	70	5.0	708	4	US-09-455-962-2	Sequence 2, Appli
257	71	5.1	466	4	US-09-328-352-7117	Sequence 7117, Ap	330	70	5.0	708	5	FCT-US95-08530-2	Sequence 2, Appli
258	71	5.1	502	1	US-08-278-635B-7	Sequence 7, Appli	331	70	5.0	1028	4	US-09-328-352-5749	Sequence 5749, Ap
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262	71	5.1	502	3	US-08-467-574-8	Sequence 8, Appli	335	70	5.0	2105	3	US-08-772-512A-3	Sequence 3, Appli
263	71	5.1	502	3	US-08-471-961-7	Sequence 7, Appli	336	70	5.0	2105	4	US-09-428-371-3	Sequence 3, Appli
264	71	5.1	502	3	US-09-217-345-8	Sequence 8, Appli	337	69.5	5.0	293	4	US-09-902-540-11200	Sequence 11200, A
265	71	5.1	502	4	US-08-487-596-8	Sequence 12, Appl	338	69.5	5.0	308	4	US-09-595-386-3	Sequence 3, Appli
266	71	5.1	502	4	US-08-345-109C-7	Sequence 7, Appli	339	69.5	5.0	308	4	US-09-993-525-3	Sequence 3, Appli
267	71	5.1	502	4	US-09-892-985-8	Sequence 8, Appli	340	69.5	5.0	345	4	US-09-543-681A-7546	Sequence 7546, Ap
268	71	5.1	502	4	US-09-578-250-2	Sequence 2, Appli	341	69.5	5.0	350	4	US-09-540-236-2338	Sequence 2338, Ap
269	71	5.1	502	4	US-09-579-250-10	Sequence 10, Appl	342	69.5	5.0	406	4	US-09-328-352-7149	Sequence 7149, Ap
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271	71	5.1	594	4	US-09-650-324A-59	Sequence 59, Appl	344	69.5	5.0	460	4	US-09-489-039A-13505	Sequence 13505, A
272	71	5.1	627	4	US-09-902-540-15743	Sequence 15743, A	345	69.5	5.0	460	4	US-08-362-512A-4	Sequence 4, Appli
273	71	5.1	658	2	US-08-825-558-4	Sequence 4, Appli	346	69.5	5.0	493	1	US-08-964-339-4	Sequence 4, Appli
274	71	5.1	658	3	US-09-312-611-4	Sequence 4, Appli	347	69.5	5.0	493	3	US-09-854-774-4	Sequence 4, Appli
275	71	5.1	859	4	US-09-313-942-7	Sequence 7, Appli	348	69.5	5.0	493	4	US-09-252-991A-28456	Sequence 28456, A
276	71	5.1	918	2	US-08-825-558-6	Sequence 6, Appli	349	69.5	5.0	501	4	US-09-122-230-7	Sequence 7, Appli
277	71	5.1	918	3	US-09-312-611-6	Sequence 6, Appli	350	69.5	5.0	513	2	US-09-540-236-2483	Sequence 2483, Ap
278	71	5.1	918	4	US-09-853-180B-3	Sequence 3, Appli	351	69.5	5.0	530	4	US-09-643-657-15	Sequence 15, Appl
279	71	5.1	922	4	US-09-569-611C-41	Sequence 41, Appl	352	69.5	5.0	591	4	US-09-538-092-760	Sequence 760, App
280	71	5.1	951	4	US-09-313-942-9	Sequence 9, Appli	353	69.5	5.0	627	4	US-07-782-298-2	Sequence 2, Appli
281	71	5.1	971	4	US-09-868-572A-1	Sequence 1, Appli	354	69.5	5.0	653	1	US-09-543-681A-4896	Sequence 3, Appli
282	70.5	5.1	186	4	US-09-134-000C-4337	Sequence 4337, Ap	355	69.5	5.0	688	4	US-09-969-362-3	Sequence 3, Appli
283	70.5	5.1	250	4	US-09-248-796A-17897	Sequence 17897, A	356	69.5	5.0	1277	3	US-09-328-352-7032	Sequence 7032, Ap
284	70.5	5.1	319	3	US-09-130-749-2	Sequence 2, Appli	357	69.5	5.0	1277	3	US-09-438-185A-313	Sequence 313, App
285	70.5	5.1	319	3	US-09-130-749-2	Sequence 2, Appli	358	69	5.0	1114	3	US-09-902-540-11124	Sequence 11124, A
286	70.5	5.1	319	4	US-09-170-436D-60	Sequence 60, Appl	359	69	5.0	114	4	US-09-198-452A-606	Sequence 606, App
287	70.5	5.1	386	4	US-09-949-016-10000	Sequence 10000, A	360	69	5.0	241	4	US-09-438-185A-569	Sequence 569, App
288	70.5	5.1	387	4	US-09-489-039A-12240	Sequence 12240, A	361	69	5.0	292	4	US-08-827-291A-2	Sequence 2, Appli
289	70.5	5.1	395	4	US-09-543-681A-6203	Sequence 6203, Ap	362	69	5.0	292	4	US-10-121-757B-20	Sequence 20, Appl
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291	70.5	5.1	420	3	US-09-134-001C-3805	Sequence 3805, Ap	364	69	5.0	308	4	US-09-328-352-7357	Sequence 7357, Ap
292	70.5	5.1	443	4	US-09-489-039A-8166	Sequence 8166, Ap	365	69	5.0	308	4	US-09-489-039A-9921	Sequence 9921, Ap
293	70.5	5.1	444	4	US-09-328-352-5249	Sequence 1, Appli	366	69	5.0	346	2	US-09-248-796A-20349	Sequence 20349, A
294	70.5	5.1	454	2	US-08-748-485-1	Sequence 1, Appli	367	69	5.0	380	1	US-09-134-000C-4234	Sequence 4234, Ap
295	70.5	5.1	467	4	US-09-107-532A-6175	Sequence 6175, Ap	368	69	5.0	380	2	US-09-540-236-2360	Sequence 2360, Ap
296	70.5	5.1	472	4	US-09-934-899-30	Sequence 10, Appl	369	69	5.0	397	4	US-09-489-039A-9921	Sequence 9921, Ap
297	70.5	5.1	472	4	US-09-934-898-30	Sequence 30, Appl	370	69	5.0	403	4	US-09-328-352-5907	Sequence 5907, Ap
298	70.5	5.1	473	4	US-09-949-016-11735	Sequence 11735, A	371	69	5.0	403	4	US-09-248-796A-20349	Sequence 20349, A
299	70.5	5.1	474	4	US-09-486-192-4	Sequence 4, Appli	372	69	5.0	446	4	US-09-134-000C-4234	Sequence 4234, Ap
300	70.5	5.1	500	4	US-09-489-039A-10995	Sequence 10995, A	373	69	5.0	483	4	US-09-540-236-2360	Sequence 2360, Ap
301	70.5	5.1	619	4	US-09-248-796A-20837	Sequence 20837, A	374	69	5.0	506	4	US-09-489-039A-13918	Sequence 13918, A
302	70.5	5.1	669	4	US-09-949-016-6720	Sequence 6720, Ap	375	69	5.0	520	4	US-09-328-352-6274	Sequence 6274, Ap
303	70.5	5.1	681	4	US-09-248-796A-20121	Sequence 20121, A	376	69	5.0	593	4	US-08-215-805A-80	Sequence 80, Appl
304	70.5	5.1	877	1	US-08-072-574-12	Sequence 12, Appl	377	69	5.0	642	4	US-09-112-096-15	Sequence 15, Appl
305	70.5	5.1	955	4	US-09-252-991A-18882	Sequence 18882, A	378	69	5.0	719	4	US-09-636-215-778	Sequence 778, App
306	70.5	5.1	1134	3	US-08-726-214-2	Sequence 2, Appli	379	69	5.0	854	3	US-09-685-166A-778	Sequence 778, App
307	70.5	5.1	1134	4	US-09-245-039-2	Sequence 2, Appli	380	69	5.0	934	1	US-09-679-426-778	Sequence 778, App
308	70.5	5.1	1788	2	US-08-962-284-2	Sequence 2, Appli	381	69	5.0	1095	3	US-09-651-236-778	Sequence 778, App
309	70	5.0	139	4	US-09-489-039A-8585	Sequence 8585, Ap	382	69	5.0	1095	4	US-08-072-574-10	Sequence 10, Appl
310	70	5.0	235	4	US-09-252-991A-19945	Sequence 19945, A	383	69	5.0	1095	4	US-08-072-574-10	Sequence 10, Appl
311	70	5.0	296	4	US-09-328-352-7482	Sequence 7482, Ap	384	69	5.0	1095	4	US-09-543-681A-5538	Sequence 5538, Ap
312	70	5.0	314	4	US-09-543-681A-6497	Sequence 6497, Ap	385	69	5.0	1095	4	US-08-466-033-15	Sequence 15, Appl
313	70	5.0	429	3	US-09-156-809-1	Sequence 1, Appli	386	69	5.0	1095	4	US-08-638-911A-2	Sequence 2, Appli
314	70	5.0	429	4	US-10-006-915-1	Sequence 1, Appli	387	69	5.0	1180	1	US-08-444-733-15	Sequence 15, Appl
315	70	5.0	492	4	US-09-328-352-6875	Sequence 6875, Ap	388	69	5.0	1212	1		
316	70	5.0	496	4	US-09-489-039A-8772	Sequence 8772, Ap	389	69	5.0	2037	4		
317	70	5.0	502	3	US-08-771-737-2	Sequence 2, Appli	390	69	5.0	2873	1		
318	70	5.0	502	4	US-09-954-936-2	Sequence 2, Appli	391	69	5.0	2873	1		
319	70	5.0	526	4	US-09-543-681A-6494	Sequence 6494, Ap	392	69	5.0	2873	2		

393	69	5.0	2873	2	US-08-464-134-15	Sequence 15, Appl	466	67.5	4.8	317	4	US-09-489-039A-9602	Sequence 9602, Ap
394	69	5.0	2873	2	US-08-461-361-15	Sequence 15, Appl	467	67.5	4.8	323	4	US-09-107-532A-5460	Sequence 5460, Ap
395	69	5.0	2873	2	US-08-485-310-15	Sequence 15, Appl	468	67.5	4.8	327	4	US-09-543-681A-6219	Sequence 6219, Ap
396	69	5.0	2873	5	FCT-US95-06266-15	Sequence 15, Appl	469	67.5	4.8	336	1	US-08-332-312-4	Sequence 4, Appl
397	68.5	4.9	180	4	US-09-270-767-32589	Sequence 32589, A	470	67.5	4.8	360	4	US-09-949-016-10048	Sequence 10048, A
398	68.5	4.9	180	4	US-09-270-767-47806	Sequence 47806, A	471	67.5	4.8	411	4	US-09-328-352-5039	Sequence 5039, Ap
399	68.5	4.9	241	2	US-08-825-781-3	Sequence 3, Appl	472	67.5	4.8	421	4	US-09-198-452A-932	Sequence 932, App
400	68.5	4.9	264	3	US-09-724-864-64	Sequence 54, Appl	473	67.5	4.8	421	4	US-09-438-185A-869	Sequence 869, App
401	68.5	4.9	300	4	US-09-489-039A-10701	Sequence 10701, A	474	67.5	4.8	425	4	US-09-134-000C-5971	Sequence 5971, Ap
402	68.5	4.9	365	4	US-09-902-540-14946	Sequence 14946, A	475	67.5	4.8	484	4	US-09-252-991A-32299	Sequence 32299, A
403	68.5	4.9	396	4	US-09-107-532A-4277	Sequence 4277, Ap	476	67.5	4.8	536	4	US-09-107-532A-5507	Sequence 5507, Ap
404	68.5	4.9	400	3	US-09-134-001C-2912	Sequence 2912, Ap	477	67.5	4.8	586	4	US-09-252-991A-24994	Sequence 24994, A
405	68.5	4.9	405	4	US-09-543-681A-6109	Sequence 6109, Ap	478	67.5	4.8	612	4	US-09-248-796A-18040	Sequence 18040, A
406	68.5	4.9	412	3	US-09-134-001C-4885	Sequence 4885, Ap	479	67.5	4.8	625	4	US-09-902-540-15330	Sequence 15330, A
407	68.5	4.9	427	4	US-09-252-991A-29948	Sequence 29948, A	480	67.5	4.8	632	4	US-09-949-016-10386	Sequence 10386, A
408	68.5	4.9	428	4	US-09-328-352-5543	Sequence 5543, Ap	481	67.5	4.8	662	4	US-09-583-110-5119	Sequence 5119, Ap
409	68.5	4.9	459	4	US-09-583-110-5017	Sequence 5017, Ap	482	67.5	4.8	664	4	US-09-107-433-2775	Sequence 2775, Ap
410	68.5	4.9	465	4	US-09-489-039A-7435	Sequence 7435, Ap	483	67.5	4.8	667	1	US-07-879-617A-8	Sequence 8, Appl
411	68.5	4.9	470	4	US-09-107-433-4341	Sequence 4341, Ap	484	67.5	4.8	667	1	US-08-753-985-8	Sequence 8, Appl
412	68.5	4.9	480	4	US-09-305-681-2	Sequence 2, Appl	485	67.5	4.8	680	4	US-09-720-317A-18	Sequence 18, Appl
413	68.5	4.9	511	4	US-09-305-681-6	Sequence 6, Appl	486	67.5	4.8	693	4	US-09-949-016-9666	Sequence 9666, Ap
414	68.5	4.9	538	4	US-09-252-991A-23060	Sequence 23060, A	487	67.5	4.8	767	4	US-09-328-352-4613	Sequence 4613, Ap
415	68.5	4.9	541	4	US-09-976-594-931	Sequence 931, App	488	67.5	4.8	912	3	US-08-617-785-2	Sequence 2, Appl
416	68.5	4.9	549	4	US-09-248-796A-20436	Sequence 20436, A	489	67.5	4.8	912	3	US-09-641-318-2	Sequence 2, Appl
417	68.5	4.9	1091	3	US-09-306-595C-7	Sequence 7, Appl	490	67.5	4.8	912	4	US-09-817-464-2	Sequence 2, Appl
418	68.5	4.9	1091	4	US-09-925-388-7	Sequence 7, Appl	491	67.5	4.8	940	4	US-09-328-352-8165	Sequence 8165, Ap
419	68.5	4.9	2104	2	US-08-808-793-4	Sequence 4, Appl	492	67.5	4.8	1084	4	US-09-221-013A-8	Sequence 8, Appl
420	68.5	4.9	2104	3	US-08-772-512A-4	Sequence 4, Appl	493	67.5	4.8	1326	4	US-09-328-352-4886	Sequence 4886, Ap
421	68.5	4.9	2104	4	US-09-428-371-4	Sequence 4, Appl	494	67	4.8	148	4	US-09-270-767-39883	Sequence 39883, A
422	68.5	4.9	313	4	US-09-693-205A-10	Sequence 10, Appl	495	67	4.8	148	4	US-09-270-767-55100	Sequence 55100, A
423	68	4.9	3559	4	US-09-858-207A-299	Sequence 299, App	496	67	4.8	162	4	US-09-270-767-45268	Sequence 45268, A
424	68	4.9	253	3	US-08-858-207A-299	Sequence 299, App	497	67	4.8	184	4	US-09-795-926-46	Sequence 46, Appl
425	68	4.9	279	4	US-09-602-787A-658	Sequence 658, App	498	67	4.8	205	4	US-09-252-991A-28363	Sequence 28363, A
426	68	4.9	309	4	US-09-710-279-42	Sequence 42, Appl	499	67	4.8	217	4	US-09-134-000C-6287	Sequence 6287, Ap
427	68	4.9	315	4	US-09-583-110-4236	Sequence 4236, Ap	500	67	4.8	225	4	US-09-543-681A-7698	Sequence 7698, Ap
428	68	4.9	355	4	US-09-107-433-3706	Sequence 3706, Ap	501	67	4.8	277	4	US-09-489-039A-10481	Sequence 10481, A
429	68	4.9	379	4	US-09-826-509-475	Sequence 475, App	502	67	4.8	290	4	US-09-248-796A-20347	Sequence 20347, A
430	68	4.9	404	4	US-09-252-991A-27854	Sequence 27854, A	503	67	4.8	306	4	US-09-489-039A-10023	Sequence 10023, A
431	68	4.9	466	4	US-09-328-352-8182	Sequence 8182, Ap	504	67	4.8	326	4	US-09-543-681A-6673	Sequence 6673, Ap
432	68	4.9	470	4	US-09-603-208A-236	Sequence 236, App	505	67	4.8	345	4	US-09-248-796A-20118	Sequence 20118, A
433	68	4.9	476	4	US-09-328-352-6673	Sequence 6673, Ap	506	67	4.8	359	4	US-09-425-488-2	Sequence 2, Appl
434	68	4.9	484	3	US-09-134-001C-5063	Sequence 5063, Ap	507	67	4.8	360	4	US-09-489-039A-8125	Sequence 8125, Ap
435	68	4.9	486	3	US-09-134-001C-3593	Sequence 3593, Ap	508	67	4.8	375	4	US-09-543-681A-4465	Sequence 4465, Ap
436	68	4.9	503	4	US-09-248-796A-16650	Sequence 16650, A	509	67	4.8	382	4	US-09-489-039A-10783	Sequence 10783, A
437	68	4.9	548	4	US-09-328-352-6605	Sequence 6605, Ap	510	67	4.8	414	3	US-09-334-601-4	Sequence 4, Appl
438	68	4.9	605	4	US-09-583-110-4773	Sequence 4773, Ap	511	67	4.8	453	1	US-08-439-131A-5	Sequence 5, Appl
439	68	4.9	619	4	US-09-540-236-2377	Sequence 2377, Ap	512	67	4.8	453	1	US-08-440-674-4	Sequence 4, Appl
440	68	4.9	633	4	US-09-328-352-5439	Sequence 5439, Ap	513	67	4.8	453	3	US-09-097-889-22	Sequence 22, Appl
441	68	4.9	638	1	US-08-295-814E-13	Sequence 13, Appl	514	67	4.8	459	3	US-09-098-079-22	Sequence 22, Appl
442	68	4.9	638	1	US-08-240-783B-2	Sequence 2, Appl	515	67	4.8	459	4	US-09-252-991A-19135	Sequence 19135, A
443	68	4.9	638	3	US-09-084-813-2	Sequence 2, Appl	516	67	4.8	465	4	US-09-489-039A-9369	Sequence 9369, Ap
444	68	4.9	638	3	US-09-343-361-13	Sequence 13, Appl	517	67	4.8	482	4	US-09-328-352-5310	Sequence 5310, Ap
445	68	4.9	638	5	FCT-US92-09662-2	Sequence 2, Appl	518	67	4.8	490	4	US-09-489-039A-8154	Sequence 8154, Ap
446	68	4.9	640	3	US-09-627-376-16	Sequence 16, Appl	519	67	4.8	494	4	US-09-328-352-7155	Sequence 7155, Ap
447	68	4.9	640	4	US-10-047-676B-16	Sequence 16, Appl	520	67	4.8	505	4	US-09-134-000C-6170	Sequence 6170, Ap
448	68	4.9	672	4	US-09-543-681A-5976	Sequence 5976, Ap	521	67	4.8	506	4	US-09-719-919A-17	Sequence 17, Appl
449	68	4.9	694	4	US-09-248-796A-20210	Sequence 20210, A	522	67	4.8	519	4	US-09-716-123-54	Sequence 54, Appl
450	68	4.9	727	4	US-09-543-681A-6690	Sequence 6690, Ap	523	67	4.8	541	4	US-09-902-540-10576	Sequence 10576, A
451	68	4.9	783	4	US-09-165-396-2	Sequence 2, Appl	524	67	4.8	545	4	US-09-543-681A-4994	Sequence 4994, Ap
452	68	4.9	905	4	US-09-538-092-1079	Sequence 1079, Ap	525	67	4.8	548	4	US-09-540-236-2286	Sequence 2286, Ap
453	68	4.9	1024	4	US-09-562-737-87	Sequence 87, Appl	526	67	4.8	576	4	US-09-902-540-14944	Sequence 14944, A
454	68	4.9	2864	4	US-08-469-260A-394	Sequence 394, App	527	67	4.8	590	4	US-09-134-000C-5783	Sequence 5783, Ap
455	68	4.9	2864	4	US-08-488-446-394	Sequence 394, App	528	67	4.8	601	4	US-09-489-039A-12897	Sequence 12897, A
456	68	4.9	2864	4	US-08-467-344A-394	Sequence 394, App	529	67	4.8	774	4	US-09-328-352-5361	Sequence 5361, Ap
457	68	4.9	2864	4	US-08-424-550B-394	Sequence 394, App	530	67	4.8	1439	2	US-08-449-644-2	Sequence 2, Appl
458	67.5	4.8	181	4	US-09-270-767-33574	Sequence 33574, A	531	67	4.8	1439	2	US-08-087-244A-2	Sequence 2, Appl
459	67.5	4.8	196	3	US-09-383-586-11	Sequence 11, Appl	532	67	4.8	1439	2	US-08-652-971-3	Sequence 3, Appl
460	67.5	4.8	196	4	US-09-823-038A-11	Sequence 11, Appl	533	67	4.8	1457	2	US-08-449-644-1	Sequence 1, Appl
461	67.5	4.8	240	4	US-09-540-236-2487	Sequence 2487, Ap	534	67	4.8	1457	2	US-08-087-244A-1	Sequence 1, Appl
462	67.5	4.8	249	4	US-09-949-016-7192	Sequence 7192, Ap	535	67	4.8	1457	2	US-08-991-258A-3	Sequence 3, Appl
463	67.5	4.8	264	4	US-09-270-767-41787	Sequence 41787, A	536	67	4.8	1457	2	US-08-769-399-3	Sequence 3, Appl
464	67.5	4.8	265	4	US-09-248-796A-17984	Sequence 17984, A	537	67	4.8	1457	3	US-08-991-953A-3	Sequence 3, Appl
465	67.5	4.8	304	4	US-09-328-352-6103	Sequence 6103, Ap	538	67	4.8	1457			

539	66.5	4.8	175	4	US-09-583-110-4664	Sequence 4564, Ap	612	4.7	483	4	US-09-107-532A-1123	Sequence 4123, Ap
540	66.5	4.8	179	4	US-09-107-433-4882	Sequence 4882, Ap	613	4.7	486	4	US-09-489-039A-7706	Sequence 7706, Ap
541	66.5	4.8	243	3	US-09-134-001C-4114	Sequence 4114, Ap	614	4.7	508	4	US-09-328-352-6467	Sequence 6467, Ap
542	66.5	4.8	249	3	US-08-858-207A-309	Sequence 309, App	615	4.7	511	1	US-08-278-635B-8	Sequence 8, Appli
543	66.5	4.8	249	4	US-09-270-767-38186	Sequence 38186, A	616	4.7	511	3	US-08-464-258B-8	Sequence 8, Appli
544	66.5	4.8	249	4	US-09-270-767-53403	Sequence 53403, A	617	4.7	511	3	US-08-471-961-8	Sequence 8, Appli
545	66.5	4.8	256	4	US-09-489-039A-9057	Sequence 9057, Ap	618	4.7	511	4	US-09-345-109C-8	Sequence 8, Appli
546	66.5	4.8	300	4	US-09-393-634-19	Sequence 19, Appl	619	4.7	536	4	US-09-270-767-44004	Sequence 44004, A
547	66.5	4.8	319	4	US-09-170-496D-196	Sequence 196, App	620	4.7	619	4	US-09-578-441-3	Sequence 3, Appli
548	66.5	4.8	324	4	US-09-543-681A-6241	Sequence 6241, Ap	621	4.7	620	4	US-09-578-441-4	Sequence 4, Appli
549	66.5	4.8	343	4	US-09-543-681A-6853	Sequence 6853, Ap	622	4.7	639	3	US-09-134-001C-5661	Sequence 5661, Ap
550	66.5	4.8	349	4	US-09-491-577-96	Sequence 96, Appl	623	4.7	687	3	US-08-834-467-2	Sequence 2, Appli
551	66.5	4.8	380	4	US-09-949-016-10856	Sequence 10856, A	624	4.7	687	3	US-09-396-177-2	Sequence 2, Appli
552	66.5	4.8	392	4	US-09-603-208A-134	Sequence 134, App	625	4.7	687	4	US-09-248-796A-14715	Sequence 14715, A
553	66.5	4.8	412	4	US-09-710-279-368	Sequence 368, App	626	4.7	748	4	US-09-902-540-13877	Sequence 13877, A
554	66.5	4.8	415	4	US-09-489-039A-10457	Sequence 10457, A	627	4.7	986	4	US-09-248-796A-19088	Sequence 19088, A
555	66.5	4.8	425	4	US-09-543-681A-7042	Sequence 7042, Ap	628	4.7	1216	4	US-09-248-796A-19646	Sequence 19646, A
556	66.5	4.8	444	4	US-09-694-519-6	Sequence 6, Appli	629	4.7	4377	4	US-09-949-016-6978	Sequence 6978, Ap
557	66.5	4.8	456	4	US-09-328-352-5446	Sequence 5446, Ap	630	65.5	157	4	US-09-461-325-155	Sequence 155, App
558	66.5	4.8	470	2	US-08-959-011-1	Sequence 1, Appli	631	65.5	157	4	US-10-012-542-155	Sequence 155, App
559	66.5	4.8	488	3	US-09-801-052-5	Sequence 5, Appli	632	65.5	157	4	US-10-115-123-155	Sequence 155, App
560	66.5	4.8	488	4	US-10-020-121-5	Sequence 5, Appli	633	65.5	160	4	US-09-270-767-46920	Sequence 46920, A
561	66.5	4.8	511	4	US-09-328-352-6365	Sequence 6365, Ap	634	65.5	195	4	US-09-489-039A-7897	Sequence 7897, Ap
562	66.5	4.8	515	4	US-09-489-039A-8402	Sequence 8402, Ap	635	65.5	267	4	US-09-198-452A-231	Sequence 231, App
563	66.5	4.8	525	4	US-09-252-991A-23870	Sequence 23870, A	636	65.5	270	4	US-09-270-767-44001	Sequence 44001, A
564	66.5	4.8	534	4	US-09-107-532A-6592	Sequence 6592, Ap	637	65.5	292	3	US-09-372-422A-4	Sequence 4, Appli
565	66.5	4.8	535	4	US-09-107-532A-6593	Sequence 6593, Ap	638	65.5	305	4	US-09-107-433-3400	Sequence 3400, Ap
566	66.5	4.8	536	4	US-09-809-665A-71	Sequence 71, Appli	639	65.5	310	3	US-09-328-352-8117	Sequence 8117, Ap
567	66.5	4.8	598	4	US-09-107-532A-7027	Sequence 7027, Ap	640	65.5	323	3	US-09-134-001C-4635	Sequence 4635, Ap
568	66.5	4.8	648	4	US-09-583-110-2729	Sequence 2729, Ap	641	65.5	329	3	US-09-740-035-2	Sequence 2, Appli
569	66.5	4.8	670	4	US-09-107-433-4919	Sequence 4919, Ap	642	65.5	339	3	US-09-710-279-1942	Sequence 1942, Ap
570	66.5	4.8	676	4	US-09-198-452A-836	Sequence 836, App	643	65.5	344	3	US-09-134-001C-5567	Sequence 5567, Ap
571	66.5	4.8	688	4	US-09-720-317A-2	Sequence 2, Appli	644	65.5	355	1	US-08-153-848-32	Sequence 32, Appli
572	66.5	4.8	719	4	US-09-438-185A-788	Sequence 788, App	645	65.5	355	3	US-08-153-848-32	Sequence 32, Appli
573	66.5	4.8	736	4	US-09-107-532A-6007	Sequence 6007, Ap	646	65.5	355	3	US-09-299-843A-28	Sequence 28, Appli
574	66.5	4.8	737	4	US-09-583-110-4038	Sequence 4038, Ap	647	65.5	355	3	US-09-299-843A-32	Sequence 32, Appli
575	66.5	4.8	738	4	US-09-328-352-4315	Sequence 4315, Ap	648	65.5	355	3	US-09-088-337B-28	Sequence 28, Appli
576	66.5	4.8	742	4	US-09-107-433-3626	Sequence 3626, Ap	649	65.5	355	3	US-09-088-337B-32	Sequence 32, Appli
577	66.5	4.8	755	4	US-09-489-039A-9089	Sequence 9089, Ap	650	65.5	355	4	US-09-170-496D-130	Sequence 130, App
578	66.5	4.8	865	4	US-09-252-991A-19339	Sequence 19339, A	651	65.5	355	4	US-09-170-496D-232	Sequence 232, App
579	66.5	4.8	899	4	US-09-437-568A-48	Sequence 48, Appl	652	65.5	355	4	US-09-317-254-68	Sequence 68, Appl
580	66.5	4.8	921	1	US-07-718-575-14	Sequence 14, Appl	653	65.5	355	5	PCT-US93-11153-28	Sequence 28, Appl
581	66.5	4.8	921	2	US-08-481-206-14	Sequence 14, Appl	654	65.5	355	5	PCT-US93-11153-32	Sequence 32, Appl
582	66.5	4.8	921	2	US-08-486-269A-14	Sequence 14, Appl	655	65.5	356	4	US-09-107-532A-4245	Sequence 4245, Ap
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584	66.5	4.8	1167	3	US-09-088-037-6	Sequence 6, Appli	657	65.5	391	4	US-09-543-681A-7029	Sequence 7029, Ap
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586	66.5	4.8	1684	3	US-08-665-259-25	Sequence 25, Appl	659	65.5	393	4	US-09-351-150A-29	Sequence 29, Appl
587	66.5	4.8	1684	3	US-08-762-500-25	Sequence 25, Appl	660	65.5	399	4	US-09-328-352-8043	Sequence 8043, Ap
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589	66.5	4.8	1704	4	US-09-032-438C-120	Sequence 120, App	662	65.5	422	4	US-09-809-665A-73	Sequence 73, Appli
590	66.5	4.8	1766	4	US-09-949-016-10796	Sequence 10796, A	663	65.5	426	6	5268463-8	Patent No. 5268463
591	66	4.7	171	3	US-09-107-383-16	Sequence 16, Appl	664	65.5	426	6	5268463-8	Patent No. 5268463
592	66	4.7	171	4	US-09-643-914-16	Sequence 16, Appl	665	65.5	427	4	US-09-438-185A-217	Sequence 217, App
593	66	4.7	171	4	US-09-742-361A-16	Sequence 16, Appl	666	65.5	428	1	US-08-570-157-5	Sequence 5, Appli
594	66	4.7	191	4	US-09-443-041A-24	Sequence 24, Appl	667	65.5	428	3	US-08-029-170-31	Sequence 31, Appl
595	66	4.7	254	4	US-09-902-540-15766	Sequence 15766, A	668	65.5	428	3	US-09-076-510-5	Sequence 5, Appli
596	66	4.7	260	4	US-09-443-041A-10	Sequence 10, Appl	669	65.5	428	4	US-09-004-349-5	Sequence 5, Appli
597	66	4.7	281	3	US-09-134-001C-4763	Sequence 134, App	670	65.5	428	4	US-09-443-745-31	Sequence 31, Appl
598	66	4.7	345	4	US-09-252-991A-28113	Sequence 28113, A	671	65.5	437	4	US-09-489-039A-8958	Sequence 8958, Ap
599	66	4.7	355	2	US-08-846-762-93	Sequence 93, Appl	672	65.5	444	1	US-07-937-609-14	Sequence 14, Appl
600	66	4.7	367	3	US-09-134-001C-5557	Sequence 5557, Ap	673	65.5	444	3	US-08-029-170-14	Sequence 14, Appl
601	66	4.7	393	3	US-09-134-001C-5594	Sequence 5594, Ap	674	65.5	444	4	US-09-443-745-14	Sequence 14, Appl
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603	66	4.7	400	4	US-09-438-185A-291	Sequence 291, App	676	65.5	457	4	US-09-151-957-6	Sequence 6, Appli
604	66	4.7	403	4	US-09-489-039A-11910	Sequence 11910, A	677	65.5	465	4	US-09-328-352-5222	Sequence 5222, Ap
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606	66	4.7	415	3	US-09-531-857A-6	Sequence 6, Appli	679	65.5	511	4	US-09-305-681-4	Sequence 4, Appli
607	66	4.7	431	5	PCT-US91-00309-6	Sequence 6, Appli	680	65.5	511	3	US-09-134-001C-4510	Sequence 4510, Ap
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609	66	4.7	439	4	US-09-248-796A-20082	Sequence 20082, A	682	65.5	600	4	US-09-438-185A-1013	Sequence 1013, Ap
610	66	4.7	464	4	US-09-252-991A-18525	Sequence 18525, A	683	65.5	601	1	US-07-676-174A-2	Sequence 2, Appli
611	66	4.7	471	4	US-09-543-681A-5580	Sequence 5580, Ap	684	65.5	697	4	US-09-603-208A-226	Sequence 226, App

685	65.5	4.7	881	4	US-09-949-016-7764	Sequence 7764, Ap	758	65	4.7	541	3	US-08-888-077A-21	Sequence 21, Appl
686	65.5	4.7	908	3	US-08-855-146-2	Sequence 2, Appli	759	65	4.7	541	3	US-09-124-698-166	Sequence 166, App
687	65.5	4.7	1036	2	US-09-180-439-8	Sequence 8, Appli	760	65	4.7	541	3	US-09-127-480-166	Sequence 166, App
688	65.5	4.7	1036	2	US-08-720-484A-5	Sequence 5, Appli	761	65	4.7	541	3	US-09-124-523-166	Sequence 166, App
689	65.5	4.7	1036	3	US-08-953-823A-5	Sequence 5, Appli	762	65	4.7	541	4	US-09-636-796A-166	Sequence 166, App
690	65.5	4.7	1036	4	US-09-398-239-5	Sequence 5, Appli	763	65	4.7	541	4	US-09-949-016-11075	Sequence 11075, A
691	65.5	4.7	1036	4	US-09-560-876A-5	Sequence 5, Appli	764	65	4.7	545	4	US-09-198-452A-519	Sequence 519, App
692	65.5	4.7	1065	4	US-09-560-876A-6	Sequence 6, Appli	765	65	4.7	545	4	US-09-438-185A-483	Sequence 483, App
693	65	4.7	139	4	US-09-902-540-14543	Sequence 14543, A	766	65	4.7	562	4	US-09-328-353-4694	Sequence 4694, Ap
694	65	4.7	144	3	US-09-134-001C-3102	Sequence 3102, Ap	767	65	4.7	574	4	US-09-107-433-3877	Sequence 3877, Ap
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696	65	4.7	168	4	US-09-544-716-15	Sequence 15, Appl	769	65	4.7	599	5	US-08-221-767-24	Sequence 24, Appl
697	65	4.7	168	4	US-09-557-921-16	Sequence 16, Appl	770	65	4.7	599	5	PCT-US95-04075-5	Sequence 2, Appli
698	65	4.7	168	4	US-09-564-357-18	Sequence 18, Appl	771	65	4.7	632	4	US-09-248-796A-20407	Sequence 20407, A
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700	65	4.7	198	3	US-09-213-293D-9	Sequence 9, Appli	773	65	4.7	738	4	US-09-107-532A-5096	Sequence 5096, Ap
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702	65	4.7	274	4	US-09-489-039A-14140	Sequence 14140, A	775	65	4.7	1095	4	US-09-636-215-780	Sequence 780, App
703	65	4.7	306	4	US-09-248-796A-17619	Sequence 17619, A	776	65	4.7	1095	4	US-09-685-166A-780	Sequence 780, App
704	65	4.7	313	2	US-08-990-379-7	Sequence 7, Appli	777	65	4.7	1095	4	US-09-679-426-780	Sequence 780, App
705	65	4.7	314	3	US-09-164-193-22	Sequence 22, Appl	778	65	4.7	1095	4	US-09-759-143-780	Sequence 780, App
706	65	4.7	314	4	US-09-221-448A-22	Sequence 22, Appl	779	65	4.7	1095	4	US-09-651-236-780	Sequence 780, App
707	65	4.7	315	4	US-09-393-634-56	Sequence 56, Appl	780	65	4.7	1104	4	US-09-793-998-11	Sequence 11, Appl
708	65	4.7	318	4	US-09-270-767-45996	Sequence 45996, A	781	65	4.7	3174	2	US-08-477-451-3	Sequence 3, Appli
709	65	4.7	331	4	US-09-252-991A-24546	Sequence 24546, A	782	64.5	4.6	173	4	US-09-270-767-33313	Sequence 33313, A
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711	65	4.7	336	4	US-09-710-279-504	Sequence 504, App	784	64.5	4.6	238	3	US-09-134-001C-3136	Sequence 3136, Ap
712	65	4.7	356	4	US-09-107-532A-6286	Sequence 6286, App	785	64.5	4.6	240	4	US-09-543-681A-5483	Sequence 5483, Ap
713	65	4.7	367	4	US-09-252-991A-31459	Sequence 31459, A	786	64.5	4.6	259	4	US-09-489-039A-11949	Sequence 11949, A
714	65	4.7	371	4	US-09-540-236-3247	Sequence 3247, Ap	787	64.5	4.6	260	3	US-08-983-075D-9	Sequence 9, Appli
715	65	4.7	380	4	US-09-489-039A-8153	Sequence 8153, Ap	788	64.5	4.6	263	4	US-09-949-016-10927	Sequence 10927, A
716	65	4.7	383	4	US-09-710-279-2026	Sequence 2026, Ap	789	64.5	4.6	276	4	US-09-583-110-5031	Sequence 5031, Ap
717	65	4.7	387	4	US-09-710-279-3180	Sequence 3180, Ap	790	64.5	4.6	284	4	US-09-107-433-3147	Sequence 3147, Ap
718	65	4.7	390	4	US-09-710-279-1422	Sequence 1422, Ap	791	64.5	4.6	323	4	US-09-489-039A-7408	Sequence 7408, Ap
719	65	4.7	393	4	US-09-134-000C-4238	Sequence 4238, Ap	792	64.5	4.6	338	4	US-09-270-767-34974	Sequence 34974, A
720	65	4.7	404	4	US-09-710-279-1204	Sequence 1204, Ap	793	64.5	4.6	338	4	US-09-270-767-50191	Sequence 50191, A
721	65	4.7	405	4	US-09-543-681A-4311	Sequence 4311, Ap	794	64.5	4.6	344	4	US-08-311-731A-172	Sequence 172, App
722	65	4.7	406	3	US-09-134-001C-4084	Sequence 4084, Ap	795	64.5	4.6	381	4	US-09-248-796A-20097	Sequence 20097, A
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724	65	4.7	423	4	US-09-824-551-2	Sequence 2, Appli	797	64.5	4.6	398	4	US-09-578-063-75	Sequence 75, Appl
725	65	4.7	426	4	US-09-252-991A-30025	Sequence 30025, A	798	64.5	4.6	399	4	US-09-328-352-7394	Sequence 7394, Ap
726	65	4.7	433	4	US-09-949-016-8065	Sequence 8065, Ap	799	64.5	4.6	404	4	US-09-489-039A-8947	Sequence 8947, Ap
727	65	4.7	436	4	US-09-583-110-4729	Sequence 4729, Ap	800	64.5	4.6	411	4	US-08-887-534A-80	Sequence 80, Appl
728	65	4.7	440	4	US-09-107-433-5201	Sequence 5201, Ap	801	64.5	4.6	411	4	US-09-527-431-80	Sequence 80, Appl
729	65	4.7	446	4	US-09-134-000C-6454	Sequence 6454, Ap	802	64.5	4.6	412	4	US-09-446-861-80	Sequence 80, Appl
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731	65	4.7	472	4	US-09-489-039A-13479	Sequence 13479, A	804	64.5	4.6	413	4	US-09-438-185A-838	Sequence 838, App
732	65	4.7	482	4	US-09-902-540-10594	Sequence 10594, A	805	64.5	4.6	416	4	US-09-540-236-2393	Sequence 2393, Ap
733	65	4.7	490	3	US-09-134-001C-5116	Sequence 5116, Ap	806	64.5	4.6	436	4	US-09-949-016-11448	Sequence 11448, A
734	65	4.7	494	4	US-09-543-681A-7033	Sequence 7033, Ap	807	64.5	4.6	439	4	US-09-710-279-2408	Sequence 2408, Ap
735	65	4.7	503	3	US-09-134-001C-3096	Sequence 3096, Ap	808	64.5	4.6	459	3	US-09-134-001C-4856	Sequence 4856, Ap
736	65	4.7	505	4	US-09-134-000C-5340	Sequence 5340, Ap	809	64.5	4.6	462	4	US-09-902-540-10036	Sequence 10036, A
737	65	4.7	515	4	US-09-489-039A-12306	Sequence 12306, A	810	64.5	4.6	470	2	US-08-724-394A-10	Sequence 10, Appl
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739	65	4.7	518	3	US-09-434-427-2	Sequence 2, Appli	812	64.5	4.6	517	4	US-09-815-923-16	Sequence 16, Appl
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741	65	4.7	518	4	US-09-548-367D-2	Sequence 2, Appli	814	64.5	4.6	539	4	US-09-518-959-8	Sequence 8, Appli
742	65	4.7	518	4	US-09-551-853D-19	Sequence 19, Appl	815	64.5	4.6	539	4	US-09-518-959-9	Sequence 9, Appli
743	65	4.7	518	4	US-09-215-450-19	Sequence 19, Appl	816	64.5	4.6	549	4	US-09-115-150-4	Sequence 4, Appli
744	65	4.7	518	4	US-09-416-901B-2	Sequence 2, Appli	817	64.5	4.6	549	4	US-09-489-039A-8237	Sequence 8237, Ap
745	65	4.7	518	4	US-09-548-376D-2	Sequence 2, Appli	818	64.5	4.6	550	4	US-09-721-870-18	Sequence 18, Appl
746	65	4.7	518	4	US-09-886-143-2	Sequence 2, Appli	819	64.5	4.6	555	4	US-09-543-681A-4582	Sequence 4582, Ap
747	65	4.7	518	4	US-09-794-927A-2	Sequence 2, Appli	820	64.5	4.6	561	4	US-09-134-000C-4759	Sequence 4759, Ap
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749	65	4.7	518	4	US-09-795-847B-2	Sequence 2, Appli	822	64.5	4.6	613	4	US-09-328-352-7962	Sequence 7962, Ap
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751	65	4.7	518	4	US-09-548-366D-2	Sequence 2, Appli	824	64.5	4.6	672	1	US-07-841-651-3	Sequence 3, Appli
752	65	4.7	518	4	US-09-548-368D-2	Sequence 2, Appli	825	64.5	4.6	674	4	US-09-540-236-3546	Sequence 3546, Ap
753	65	4.7	518	4	US-09-794-925A-2	Sequence 2, Appli	826	64.5	4.6	677	4	US-09-543-681A-6388	Sequence 6388, Ap
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756	65	4.7	541	2	US-08-967-101-166	Sequence 166, App	829	64.5	4.6	870	4	US-09-949-016-11434	Sequence 11434, A
757	65	4.7	541	2	US-08-592-541-166	Sequence 166, App	830	64.5	4.6	878	4	US-09-949-016-11109	Sequence 11109, A

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833	64.5	4.6	908	3	US-08-249-221B-6	Sequence 2, Appli	906	64	4.6	1063	4	US-09-248-796A-14361	Sequence 14361, A
834	64.5	4.6	908	4	US-09-949-016-7025	Sequence 7025, Ap	907	64	4.6	1278	4	US-09-462-136-2	Sequence 2, Appli
835	64.5	4.6	908	4	PCT-US91-09422-19	Sequence 19, Appli	908	64	4.6	1318	4	US-09-949-016-10152	Sequence 10152, A
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837	64.5	4.6	1122	4	US-09-489-039A-8554	Sequence 8554, Ap	910	63.5	4.6	175	3	US-08-858-207A-363	Sequence 363, App
838	64	4.6	1225	4	US-09-270-767-36480	Sequence 36480, A	911	63.5	4.6	221	4	US-09-248-796A-16290	Sequence 16290, A
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841	64	4.6	171	4	US-09-902-540-10737	Sequence 10737, A	914	63.5	4.6	237	3	US-08-767-820A-21	Sequence 21, Appli
842	64	4.6	179	4	US-09-902-540-11797	Sequence 11797, A	915	63.5	4.6	237	3	US-08-622-046B-1	Sequence 1, Appli
843	64	4.6	205	4	US-09-540-236-2955	Sequence 2955, Ap	916	63.5	4.6	237	3	US-09-100-264-12	Sequence 12, Appli
844	64	4.6	238	3	US-09-247-155-89	Sequence 89, Appli	917	63.5	4.6	237	4	US-08-843-076D-8	Sequence 8, Appli
845	64	4.6	250	4	US-09-543-681A-4487	Sequence 4487, Ap	918	63.5	4.6	244	3	US-08-622-046B-5	Sequence 5, Appli
846	64	4.6	258	4	US-09-328-352-4425	Sequence 4425, Ap	919	63.5	4.6	247	3	US-09-489-039A-8478	Sequence 8478, Ap
847	64	4.6	264	4	US-09-107-532A-5290	Sequence 5290, Ap	920	63.5	4.6	250	3	US-09-134-001C-4399	Sequence 4399, Ap
848	64	4.6	296	4	US-09-724-623-103	Sequence 103, App	921	63.5	4.6	250	4	US-09-949-016-10362	Sequence 10362, A
849	64	4.6	315	3	US-09-134-001C-3561	Sequence 3561, Ap	922	63.5	4.6	261	3	US-08-768-859A-19	Sequence 19, Appli
850	64	4.6	332	2	US-08-671-978A-8	Sequence 8, Appli	923	63.5	4.6	261	3	US-08-767-820A-19	Sequence 19, Appli
851	64	4.6	344	3	US-09-110-116-4	Sequence 4, Appli	924	63.5	4.6	261	3	US-08-622-046B-3	Sequence 3, Appli
852	64	4.6	355	4	US-09-170-496D-164	Sequence 164, App	925	63.5	4.6	279	4	US-09-252-991A-24283	Sequence 24283, A
853	64	4.6	369	4	US-08-462-509B-4	Sequence 4, Appli	926	63.5	4.6	288	3	US-09-372-448A-2	Sequence 2, Appli
854	64	4.6	369	5	PCT-US95-05616-4	Sequence 4, Appli	927	63.5	4.6	289	3	US-09-372-422A-2	Sequence 2, Appli
855	64	4.6	371	4	US-09-328-352-7132	Sequence 7132, Ap	928	63.5	4.6	309	4	US-09-902-540-11246	Sequence 11246, A
856	64	4.6	372	4	US-08-462-509B-6	Sequence 6, Appli	929	63.5	4.6	311	4	US-09-489-039A-13013	Sequence 13013, A
857	64	4.6	374	3	US-09-045-583-48	Sequence 48, Appli	930	63.5	4.6	328	4	US-09-489-039A-10986	Sequence 10986, A
858	64	4.6	374	4	US-09-534-185-48	Sequence 48, Appli	931	63.5	4.6	332	4	US-09-252-991A-29029	Sequence 29029, A
859	64	4.6	377	5	PCT-US95-05616-6	Sequence 6, Appli	932	63.5	4.6	332	4	US-09-452-991A-31791	Sequence 31791, A
860	64	4.6	380	3	US-09-097-889-25	Sequence 25, Appli	933	63.5	4.6	345	4	US-09-248-796A-20780	Sequence 20780, A
861	64	4.6	380	4	US-09-098-079-25	Sequence 25, Appli	934	63.5	4.6	356	4	US-08-567-882-7	Sequence 7, Appli
862	64	4.6	386	4	US-09-813-133A-2	Sequence 2, Appli	935	63.5	4.6	359	4	US-09-248-796A-17633	Sequence 17633, A
863	64	4.6	386	4	US-09-248-796A-16627	Sequence 16627, A	936	63.5	4.6	378	4	US-09-540-236-3528	Sequence 3528, Ap
864	64	4.6	386	4	US-10-212-877-2	Sequence 2, Appli	937	63.5	4.6	379	1	US-08-227-108-18	Sequence 18, Appli
865	64	4.6	389	2	US-08-846-705-2	Sequence 2, Appli	938	63.5	4.6	379	2	US-09-073-674-18	Sequence 18, Appli
866	64	4.6	389	4	US-09-211-823C-23	Sequence 23, Appli	939	63.5	4.6	391	4	US-09-489-039A-9791	Sequence 9791, Ap
867	64	4.6	394	4	US-09-710-279-3292	Sequence 3292, Ap	940	63.5	4.6	404	2	US-08-428-243-7	Sequence 7, Appli
868	64	4.6	398	4	US-09-489-039A-13159	Sequence 13159, A	941	63.5	4.6	404	5	PCT-US93-10301-7	Sequence 7, Appli
869	64	4.6	402	3	US-08-846-704-4	Sequence 4, Appli	942	63.5	4.6	405	4	US-09-248-796A-17965	Sequence 17965, A
870	64	4.6	402	4	US-08-462-509B-2	Sequence 2, Appli	943	63.5	4.6	414	4	US-09-489-039A-10869	Sequence 10869, A
871	64	4.6	415	5	PCT-US95-05616-2	Sequence 2, Appli	944	63.5	4.6	430	4	US-09-583-110-4230	Sequence 4230, Ap
872	64	4.6	415	4	US-09-134-000C-4092	Sequence 4092, Ap	945	63.5	4.6	430	4	US-09-248-796A-14556	Sequence 14556, A
873	64	4.6	425	3	US-08-846-704-2	Sequence 2, Appli	946	63.5	4.6	437	4	US-09-107-433-3678	Sequence 3678, Ap
874	64	4.6	425	3	US-09-479-128-2	Sequence 2, Appli	947	63.5	4.6	449	4	US-09-949-016-8594	Sequence 8594, Ap
875	64	4.6	425	4	US-09-211-823C-22	Sequence 22, Appli	948	63.5	4.6	457	4	US-09-721-870-26	Sequence 26, Appli
876	64	4.6	425	4	US-08-826-509-349	Sequence 549, App	949	63.5	4.6	458	4	US-09-328-352-5083	Sequence 5083, Ap
877	64	4.6	428	4	US-09-345-236B-62	Sequence 62, Appli	950	63.5	4.6	470	4	US-09-543-681A-4625	Sequence 4625, Ap
878	64	4.6	430	1	US-08-601-435-2	Sequence 2, Appli	951	63.5	4.6	473	1	US-08-439-131A-4	Sequence 4, Appli
879	64	4.6	430	2	US-08-931-047-2	Sequence 2, Appli	952	63.5	4.6	473	1	US-08-440-674-3	Sequence 3, Appli
880	64	4.6	430	2	US-08-783-202-2	Sequence 2, Appli	953	63.5	4.6	476	4	US-08-879-337-7	Sequence 7, Appli
881	64	4.6	430	4	US-09-443-041A-31	Sequence 31, Appli	954	63.5	4.6	476	4	US-09-489-039A-10203	Sequence 10203, A
882	64	4.6	441	4	US-09-583-110-4400	Sequence 4400, Ap	955	63.5	4.6	482	4	US-09-328-352-7784	Sequence 7784, Ap
883	64	4.6	445	4	US-09-107-433-5039	Sequence 5039, Ap	956	63.5	4.6	488	1	US-08-115-365-2	Sequence 2, Appli
884	64	4.6	450	3	US-09-134-001C-4858	Sequence 4858, Ap	957	63.5	4.6	488	1	US-08-586-897-2	Sequence 2, Appli
885	64	4.6	450	4	US-09-252-991A-28134	Sequence 28134, A	958	63.5	4.6	488	4	US-09-826-509-561	Sequence 561, App
886	64	4.6	452	4	US-09-489-039A-12558	Sequence 12558, A	959	63.5	4.6	521	3	US-08-956-322-4	Sequence 4, Appli
887	64	4.6	458	1	US-09-041-075A-11	Sequence 11, Appli	960	63.5	4.6	531	4	US-09-489-039A-9781	Sequence 9781, Ap
888	64	4.6	476	3	US-09-134-001C-3778	Sequence 3778, Ap	961	63.5	4.6	534	4	US-09-710-279-920	Sequence 920, App
889	64	4.6	495	4	US-09-359-167-2	Sequence 2, Appli	962	63.5	4.6	542	4	US-09-630-123-2	Sequence 2, Appli
890	64	4.6	495	4	US-09-915-181A-7	Sequence 7, Appli	963	63.5	4.6	557	4	US-09-902-540-12884	Sequence 12884, A
891	64	4.6	501	4	US-09-328-352-6371	Sequence 6371, Ap	964	63.5	4.6	571	4	US-09-248-796A-20375	Sequence 20375, A
892	64	4.6	522	4	US-09-902-540-12496	Sequence 12496, A	965	63.5	4.6	600	4	US-09-902-540-14821	Sequence 14821, A
893	64	4.6	533	1	US-08-294-872-2	Sequence 2, Appli	966	63.5	4.6	650	3	US-08-800-291B-4	Sequence 4, Appli
894	64	4.6	533	5	PCT-US95-09823-2	Sequence 2, Appli	967	63.5	4.6	652	3	US-09-110-116-1	Sequence 1, Appli
895	64	4.6	536	4	US-09-359-167-8	Sequence 8, Appli	968	63.5	4.6	652	3	US-08-956-322-2	Sequence 2, Appli
896	64	4.6	585	4	US-09-949-016-7705	Sequence 7705, Ap	969	63.5	4.6	658	4	US-09-492-709A-352	Sequence 352, App
897	64	4.6	613	4	US-09-107-532A-6935	Sequence 6935, Ap	970	63.5	4.6	658	4	US-09-538-092-1190	Sequence 1190, Ap
898	64	4.6	615	4	US-09-107-532A-6507	Sequence 6507, Ap	971	63.5	4.6	685	4	US-09-720-317A-31	Sequence 31, Appli
899	64	4.6	671	4	US-09-328-352-7868	Sequence 7868, Ap	972	63.5	4.6	689	4	US-09-248-796A-15264	Sequence 15264, A
900	64	4.6	696	4	US-09-107-532A-4163	Sequence 4163, A	973	63.5	4.6	790	4	US-09-543-681A-5459	Sequence 5459, Ap
901	64	4.6	771	4	US-09-252-991A-23521	Sequence 23521, A	974	63.5	4.6	803	4	US-09-543-681A-6767	Sequence 6767, Ap
902	64	4.6	816	4	US-09-248-796A-20939	Sequence 20939, A	975	63.5	4.6	850	4	US-09-583-110-4394	Sequence 4394, Ap
903	64	4.6	823	4	US-09-949-016-6852	Sequence 6852, Ap	976	63.5	4.6	861	4	US-09-107-433-2860	Sequence 2860, Ap

977	63.5	4.6	923	3	US-09-397-885-1	Sequence 1, Appli	1050	63	4.5	683	4	US-08-979-847B-210	Sequence 210, Appl
978	63.5	4.6	923	4	US-09-969-362-1	Sequence 1, Appli	1051	63	4.5	849	3	US-08-804-439A-17	Sequence 17, Appl
979	63.5	4.6	1065	4	US-09-221-013A-10	Sequence 10, Appl	1052	63	4.5	849	3	US-08-720-229-17	Sequence 17, Appl
980	63.5	4.6	1098	3	US-08-726-214-10	Sequence 10, Appl	1053	63	4.5	852	4	US-09-319-588C-18	Sequence 18, Appl
981	63.5	4.6	1895	2	US-08-619-554-4	Sequence 4, Appli	1054	63	4.5	970	4	US-09-795-927-7	Sequence 7, Appl
982	63.5	4.6	2522	3	US-09-251-645-13	Sequence 13, Appl	1055	63	4.5	1076	4	US-10-160-719A-58	Sequence 58, Appl
983	63	4.5	138	4	US-09-583-110-4890	Sequence 4890, Ap	1056	63	4.5	1079	4	US-09-489-039A-7502	Sequence 7502, Ap
984	63	4.5	143	4	US-09-107-433-4477	Sequence 4477, Ap	1057	63	4.5	1168	4	US-09-313-942-24	Sequence 24, Appl
985	63	4.5	154	4	US-09-248-796A-20059	Sequence 20059, A	1058	63	4.5	2227	3	US-08-475-886-4	Sequence 4, Appli
986	63	4.5	175	4	US-09-543-681A-8328	Sequence 8328, Ap	1059	63	4.5	2227	3	US-08-475-886-6	Sequence 6, Appli
987	63	4.5	214	4	US-09-107-532A-5408	Sequence 5408, Ap	1060	63	4.5	2227	3	US-08-397-232-4	Sequence 4, Appli
988	63	4.5	219	1	US-08-186-529-4	Sequence 4, Appli	1061	63	4.5	2227	4	US-09-653-499-4	Sequence 4, Appli
989	63	4.5	219	1	US-08-640-386A-4	Sequence 4, Appli	1062	63	4.5	2227	4	US-09-653-499-6	Sequence 6, Appli
990	63	4.5	249	4	US-09-902-540-13089	Sequence 13089, A	1063	63	4.5	2227	4	US-10-135-988-4	Sequence 4, Appli
991	63	4.5	250	4	US-09-107-532A-6270	Sequence 6270, Ap	1064	63	4.5	2227	4	US-10-135-988-6	Sequence 6, Appli
992	63	4.5	253	1	US-08-265-087-4	Sequence 4, Appli	1065	63	4.5	2368	1	US-08-198-448B-15	Sequence 15, Appl
993	63	4.5	253	1	US-08-621-493-4	Sequence 4, Appli	1066	63	4.5	2368	2	US-08-870-693-15	Sequence 15, Appl
994	63	4.5	253	2	US-08-684-687-4	Sequence 4, Appli	1067	63	4.5	2910	1	US-08-466-033-183	Sequence 183, App
995	63	4.5	253	2	US-08-965-688-4	Sequence 4, Appli	1068	63	4.5	2910	2	US-08-444-733-183	Sequence 183, App
996	63	4.5	253	3	US-09-260-173-4	Sequence 4, Appli	1069	63	4.5	2910	2	US-08-464-134-183	Sequence 183, App
997	63	4.5	233	4	US-08-924-703-6	Sequence 6, Appli	1070	63	4.5	2910	2	US-08-461-361-183	Sequence 183, App
998	63	4.5	239	4	US-09-328-352-6237	Sequence 6237, Ap	1071	63	4.5	2910	2	US-08-485-910-183	Sequence 183, App
999	63	4.5	259	4	US-09-602-777A-292	Sequence 292, App	1072	63	4.5	2910	5	PCT-US955-06286-157	Sequence 157, App
1000	63	4.5	273	4	US-09-949-016-8333	Sequence 8333, Ap	1073	62.5	4.5	117	4	US-09-422-569-10	Sequence 10, Appl
1001	63	4.5	279	4	US-09-489-039A-13210	Sequence 13210, A	1074	62.5	4.5	117	4	US-09-823-153-2	Sequence 2, Appli
1002	63	4.5	284	4	US-09-270-767-13635	Sequence 33635, A	1075	62.5	4.5	131	4	US-09-902-540-12460	Sequence 12460, A
1003	63	4.5	284	4	US-09-270-767-48852	Sequence 48852, A	1076	62.5	4.5	164	4	US-09-902-540-10754	Sequence 10754, A
1004	63	4.5	287	4	US-09-134-000C-5944	Sequence 5944, Ap	1077	62.5	4.5	176	4	US-09-248-796A-15652	Sequence 15652, A
1005	63	4.5	289	4	US-09-540-236-2019	Sequence 2019, Ap	1078	62.5	4.5	202	3	US-09-134-001C-5617	Sequence 5617, Ap
1006	63	4.5	290	4	US-09-910-174B-8	Sequence 8, Appli	1079	62.5	4.5	234	4	US-09-543-681A-7271	Sequence 7271, Ap
1007	63	4.5	290	4	US-09-451-291-1	Sequence 1, Appli	1080	62.5	4.5	234	4	US-09-107-532A-3905	Sequence 3905, Ap
1008	63	4.5	290	4	US-09-645-069-4	Sequence 4, Appli	1081	62.5	4.5	237	4	US-09-710-279-2580	Sequence 2580, Ap
1009	63	4.5	290	4	US-09-583-110-2991	Sequence 2991, Ap	1082	62.5	4.5	237	1	US-08-096-946-10	Sequence 10, Appl
1010	63	4.5	345	4	US-09-362-123A-2	Sequence 2, Appli	1083	62.5	4.5	237	3	US-08-768-859A-16	Sequence 16, Appl
1011	63	4.5	345	4	US-09-107-532A-4426	Sequence 4426, Ap	1084	62.5	4.5	237	3	US-08-767-820A-16	Sequence 16, Appl
1012	63	4.5	346	4	US-09-149-476-493	Sequence 493, App	1085	62.5	4.5	237	3	US-08-622-046B-12	Sequence 12, Appl
1013	63	4.5	346	4	US-09-149-476-493	Sequence 493, App	1086	62.5	4.5	237	3	US-08-944-483-37	Sequence 37, Appl
1014	63	4.5	350	4	US-09-902-540-14418	Sequence 14418, A	1087	62.5	4.5	237	3	US-09-100-264-1	Sequence 1, Appli
1015	63	4.5	354	4	US-09-270-767-45297	Sequence 45297, A	1088	62.5	4.5	237	4	US-08-843-076D-1	Sequence 1, Appli
1016	63	4.5	361	4	US-09-543-681A-5180	Sequence 5180, Ap	1089	62.5	4.5	237	5	PCT-US94-07329-10	Sequence 10, Appl
1017	63	4.5	365	2	US-08-833-610-7	Sequence 7, Appli	1090	62.5	4.5	237	5	PCT-US95-06157-16	Sequence 16, Appl
1018	63	4.5	365	2	US-08-834-033A-17	Sequence 17, Appl	1091	62.5	4.5	238	3	US-08-768-859A-8	Sequence 8, Appli
1019	63	4.5	365	4	US-09-377-452-7	Sequence 7, Appli	1092	62.5	4.5	238	3	US-08-767-820A-8	Sequence 8, Appli
1020	63	4.5	374	4	US-09-721-341-8	Sequence 8, Appli	1093	62.5	4.5	238	5	PCT-US95-06157-8	Sequence 8, Appli
1021	63	4.5	374	4	US-09-721-495B-8	Sequence 8, Appli	1094	62.5	4.5	244	3	US-08-768-859A-10	Sequence 10, Appl
1022	63	4.5	387	4	US-09-543-681A-5180	Sequence 17, Appl	1095	62.5	4.5	244	3	US-08-767-820A-10	Sequence 10, Appl
1023	63	4.5	391	4	US-09-848B-17	Sequence 17, Appl	1096	62.5	4.5	244	3	US-08-622-046B-16	Sequence 16, Appl
1024	63	4.5	398	4	US-09-710-279-1236	Sequence 1236, Ap	1097	62.5	4.5	244	3	US-08-622-046B-16	Sequence 16, Appl
1025	63	4.5	401	4	US-09-328-352-6411	Sequence 6411, Ap	1098	62.5	4.5	244	3	US-09-100-264-5	Sequence 5, Appli
1026	63	4.5	422	3	US-09-489-039A-9416	Sequence 9416, Ap	1099	62.5	4.5	244	5	US-08-843-076D-5	Sequence 5, Appli
1027	63	4.5	424	4	US-09-134-001C-4048	Sequence 4048, Ap	1100	62.5	4.5	261	3	PCT-US95-06157-10	Sequence 10, Appl
1028	63	4.5	425	4	US-09-543-681A-4762	Sequence 4762, Ap	1101	62.5	4.5	261	3	US-08-768-859A-6	Sequence 6, Appli
1029	63	4.5	430	4	US-09-543-681A-6042	Sequence 6042, Ap	1102	62.5	4.5	261	3	US-08-767-820A-6	Sequence 6, Appli
1030	63	4.5	430	4	US-09-443-041A-18	Sequence 443, Ap	1103	62.5	4.5	261	3	US-08-622-046B-14	Sequence 14, Appl
1031	63	4.5	438	2	US-08-677-049-9	Sequence 4627, Ap	1104	62.5	4.5	261	3	US-09-100-264-7	Sequence 7, Appli
1032	63	4.5	443	1	US-08-570-157-6	Sequence 9, Appli	1105	62.5	4.5	261	3	US-08-983-075D-7	Sequence 7, Appli
1033	63	4.5	443	3	US-09-076-510-6	Sequence 6, Appli	1106	62.5	4.5	261	5	US-08-843-076D-3	Sequence 3, Appli
1034	63	4.5	461	1	US-09-004-349-6	Sequence 6, Appli	1107	62.5	4.5	276	3	PCT-US95-06157-6	Sequence 6, Appli
1035	63	4.5	461	1	US-08-194-338-4	Sequence 4, Appli	1108	62.5	4.5	277	1	US-09-134-001C-3456	Sequence 3456, Ap
1036	63	4.5	468	2	US-08-959-011-3	Sequence 3, Appli	1109	62.5	4.5	277	5	US-08-118-270-68	Sequence 68, Appl
1037	63	4.5	478	4	US-09-107-532A-6105	Sequence 6105, Ap	1110	62.5	4.5	278	4	PCT-US93-08528-68	Sequence 68, Appl
1038	63	4.5	478	4	US-09-949-016-6543	Sequence 6543, Ap	1111	62.5	4.5	283	4	US-09-949-016-7711	Sequence 7711, Ap
1039	63	4.5	485	4	US-09-949-016-10465	Sequence 10465, A	1112	62.5	4.5	291	4	US-09-134-000C-4870	Sequence 4870, Ap
1040	63	4.5	497	4	US-09-248-796A-20395	Sequence 20395, A	1113	62.5	4.5	291	4	US-09-393-634-64	Sequence 64, Appl
1041	63	4.5	506	4	US-09-543-681A-8246	Sequence 8246, Ap	1114	62.5	4.5	291	4	US-09-949-016-6919	Sequence 6919, Ap
1042	63	4.5	521	3	US-09-134-001C-4290	Sequence 4290, Ap	1115	62.5	4.5	292	4	US-09-543-681A-7918	Sequence 7918, Ap
1043	63	4.5	554	4	US-09-540-236-2634	Sequence 2634, Ap	1116	62.5	4.5	304	4	US-09-328-352-7098	Sequence 7098, Ap
1044	63	4.5	580	4	US-09-657-252-2	Sequence 2, Appli	1117	62.5	4.5	323	4	US-09-540-236-2883	Sequence 2883, Ap
1045	63	4.5	597	4	US-09-328-352-4703	Sequence 2, Appli	1118	62.5	4.5	324	4	US-09-543-681A-5947	Sequence 5947, Ap
1046	63	4.5	611	2	US-08-677-049-2	Sequence 2, Appli	1119	62.5	4.5	325	4	US-09-107-532A-6542	Sequence 6542, Ap
1047	63	4.5	629	4	US-09-252-991A-17988	Sequence 17988, A	1120	62.5	4.5	332	4	US-09-107-532A-6542	Sequence 6542, Ap
1048	63	4.5	659	4	US-09-252-991A-30353	Sequence 30353, A	1121	62.5	4.5	332	4	US-09-252-991A-18980	Sequence 18980, A
1049	63	4.5	683	4	US-08-979-847B-208	Sequence 208, App	1122	62.5	4.5	332	4	US-09-252-991A-31150	Sequence 31150, A
1049	63	4.5	683	4	US-08-979-847B-208	Sequence 208, App	1122	62.5	4.5	332	4	US-09-949-016-6161	Sequence 6161, Ap

1123	62.5	4.5	351	4	US-09-949-016-11252	Sequence 11252, A	1196	62.5	4.5	687	4	US-09-543-681A-5839	Sequence 5839, Ap
1124	62.5	4.5	351	4	US-09-949-016-11253	Sequence 11253, A	1197	62.5	4.5	704	4	US-09-328-352-4189	Sequence 4189, Ap
1125	62.5	4.5	355	4	US-09-328-352-4374	Sequence 4374, Ap	1198	62.5	4.5	734	4	US-09-252-991A-33036	Sequence 33036, A
1126	62.5	4.5	361	3	US-09-248-568-2	Sequence 2, Appli	1199	62.5	4.5	784	4	US-09-489-039A-14075	Sequence 14075, A
1127	62.5	4.5	361	4	US-09-364-425B-19	Sequence 19, Appl	1200	62.5	4.5	822	4	US-09-248-796A-20139	Sequence 20139, A
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1129	62.5	4.5	371	4	US-09-636-215-708	Sequence 708, App	1202	62.5	4.5	877	3	US-08-367-264-12	Sequence 12, Appl
1130	62.5	4.5	371	4	US-09-685-166A-708	Sequence 708, App	1203	62.5	4.5	877	4	US-09-153-757-12	Sequence 12, Appl
1131	62.5	4.5	371	4	US-09-679-426-708	Sequence 708, App	1204	62.5	4.5	877	4	US-09-153-757-12	Sequence 12, Appl
1132	62.5	4.5	371	4	US-09-759-143-708	Sequence 708, App	1205	62.5	4.5	883	1	US-09-459-715-12	Sequence 2, Appli
1133	62.5	4.5	371	4	US-09-651-236-708	Sequence 708, App	1206	62.5	4.5	883	3	US-08-106-433A-2	Sequence 2, Appli
1134	62.5	4.5	376	4	US-09-107-532A-7048	Sequence 7048, App	1207	62.5	4.5	889	1	US-09-254-352B-16	Sequence 16, Appl
1135	62.5	4.5	376	4	US-09-949-016-7545	Sequence 7545, Ap	1208	62.5	4.5	908	3	US-08-118-101A-4	Sequence 4, Appli
1136	62.5	4.5	380	4	US-09-149-045-2	Sequence 2, Appli	1209	62.5	4.5	908	3	US-08-823-110-1	Sequence 1, Appli
1137	62.5	4.5	382	4	US-09-252-991A-32165	Sequence 32165, A	1210	62.5	4.5	919	3	US-08-604-298-1	Sequence 2, Appli
1138	62.5	4.5	392	4	US-09-489-039A-12520	Sequence 12520, A	1211	62.5	4.5	919	3	US-08-377-503-2	Sequence 2, Appli
1139	62.5	4.5	398	4	US-09-328-352-6136	Sequence 6136, App	1212	62.5	4.5	987	4	US-08-178-019-2	Sequence 2, Appli
1140	62.5	4.5	400	4	US-09-636-215-852	Sequence 852, App	1213	62.5	4.5	1032	4	US-09-949-016-10865	Sequence 10865, A
1141	62.5	4.5	400	4	US-09-685-166A-852	Sequence 852, App	1214	62.5	4.5	1094	4	US-09-332-522B-94	Sequence 94, Appl
1142	62.5	4.5	400	4	US-09-679-426-852	Sequence 852, App	1215	62.5	4.5	1094	4	US-10-160-719A-26	Sequence 26, Appl
1143	62.5	4.5	400	4	US-09-759-143-852	Sequence 852, App	1216	62.5	4.5	1094	4	US-10-160-719A-46	Sequence 46, Appl
1144	62.5	4.5	400	4	US-09-651-236-852	Sequence 852, App	1217	62.5	4.5	1158	4	US-09-313-942-26	Sequence 26, Appl
1145	62.5	4.5	405	4	US-09-489-039A-9411	Sequence 9411, Ap	1218	62.5	4.5	1248	4	US-09-313-942-26	Sequence 2, Appli
1146	62.5	4.5	409	4	US-09-328-352-5147	Sequence 5147, Ap	1219	62.5	4.5	1278	4	US-10-042-810-4	Sequence 4, Appli
1147	62.5	4.5	415	4	US-09-603-208A-286	Sequence 286, App	1220	62.5	4.5	1338	4	US-10-042-810-4	Sequence 2, Appli
1148	62.5	4.5	424	4	US-09-489-039A-9628	Sequence 9628, Ap	1221	62.5	4.5	1765	4	US-09-270-767-45587	Sequence 45587, A
1149	62.5	4.5	437	4	US-09-248-796A-16548	Sequence 16548, A	1222	62.5	4.5	1849	4	US-08-851-567B-49	Sequence 49, Appl
1150	62.5	4.5	437	4	US-09-830-433A-59	Sequence 59, Appl	1223	62.5	4.5	2516	4	US-08-851-567B-47	Sequence 47, Appl
1151	62.5	4.5	451	4	US-09-446-861-127	Sequence 127, App	1224	62	4.5	2516	4	US-09-817-514A-2	Sequence 2, Appli
1152	62.5	4.5	451	4	US-09-925-637-22	Sequence 22, Appl	1225	62	4.5	103	4	US-09-543-681A-7951	Sequence 7951, Ap
1153	62.5	4.5	455	4	US-09-543-681A-5989	Sequence 5989, Ap	1226	62	4.5	152	4	US-09-710-279-1488	Sequence 1488, Ap
1154	62.5	4.5	458	4	US-09-489-039A-13954	Sequence 13954, A	1227	62	4.5	152	4	US-09-710-279-2224	Sequence 2224, Ap
1155	62.5	4.5	461	4	US-09-252-991A-28434	Sequence 28434, A	1228	62	4.5	159	3	US-09-134-001C-5575	Sequence 5575, Ap
1156	62.5	4.5	461	4	US-09-489-039A-9623	Sequence 9623, Ap	1229	62	4.5	175	4	US-09-902-540-11358	Sequence 11358, A
1157	62.5	4.5	465	4	US-09-328-352-4543	Sequence 4543, Ap	1230	62	4.5	186	4	US-09-583-110-2827	Sequence 2827, Ap
1158	62.5	4.5	467	3	US-08-706-344C-4	Sequence 4, Appli	1231	62	4.5	197	4	US-09-917-265A-50	Sequence 50, Appl
1159	62.5	4.5	469	4	US-09-328-352-5007	Sequence 5007, Ap	1232	62	4.5	219	4	US-09-540-236-2720	Sequence 2720, Ap
1160	62.5	4.5	480	4	US-09-266-965-17	Sequence 17, Appl	1233	62	4.5	221	4	US-09-710-279-966	Sequence 966, App
1161	62.5	4.5	484	4	US-09-352-5007	Sequence 5007, Ap	1234	62	4.5	222	4	US-09-917-265A-105	Sequence 105, App
1162	62.5	4.5	487	4	US-09-489-039A-12980	Sequence 12980, A	1235	62	4.5	222	4	US-09-917-265A-105	Sequence 105, App
1163	62.5	4.5	489	4	US-09-328-352-5330	Sequence 5330, Ap	1236	62	4.5	226	3	US-09-134-001C-5590	Sequence 5590, Ap
1164	62.5	4.5	503	4	US-09-248-796A-20120	Sequence 20120, A	1237	62	4.5	233	2	US-09-024-848-4	Sequence 4, Appli
1165	62.5	4.5	508	4	US-09-332-522E-4	Sequence 4, Appli	1238	62	4.5	233	3	US-09-348-116A-4	Sequence 4, Appli
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1168	62.5	4.5	516	4	US-09-543-681A-5385	Sequence 5385, Ap	1241	62	4.5	237	3	US-09-134-001C-3057	Sequence 3057, Ap
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1170	62.5	4.5	553	3	US-09-030-607-113	Sequence 113, App	1243	62	4.5	242	6	5455030-15	Patent No. 5455030
1171	62.5	4.5	553	3	US-09-439-313-113	Sequence 113, App	1244	62	4.5	242	6	5455030-15	Patent No. 5455030
1172	62.5	4.5	553	3	US-09-352-616A-113	Sequence 113, App	1245	62	4.5	247	4	US-09-328-352-6024	Sequence 6024, Ap
1173	62.5	4.5	553	4	US-09-602-877A-101	Sequence 101, App	1246	62	4.5	260	4	US-09-543-681A-5980	Sequence 5980, Ap
1174	62.5	4.5	553	4	US-09-232-149A-113	Sequence 113, App	1247	62	4.5	261	3	US-09-134-001C-4966	Sequence 4966, Ap
1175	62.5	4.5	553	4	US-09-819-812-113	Sequence 113, App	1248	62	4.5	265	4	US-09-489-039A-13677	Sequence 13677, A
1176	62.5	4.5	553	4	US-09-636-215-113	Sequence 113, App	1249	62	4.5	278	4	US-09-543-681A-6624	Sequence 6624, Ap
1177	62.5	4.5	553	4	US-09-685-166A-113	Sequence 113, App	1250	62	4.5	284	4	US-09-489-039A-10188	Sequence 10188, A
1178	62.5	4.5	553	4	US-09-115-453-113	Sequence 113, App	1251	62	4.5	302	4	US-09-328-352-6199	Sequence 6199, A
1179	62.5	4.5	553	4	US-09-688-489-113	Sequence 113, App	1252	62	4.5	308	4	US-09-252-991A-16800	Sequence 16800, A
1180	62.5	4.5	553	4	US-09-759-426-113	Sequence 113, App	1253	62	4.5	308	4	US-09-107-532A-6023	Sequence 6023, Ap
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1182	62.5	4.5	554	4	US-09-252-991A-27968	Sequence 27968, A	1255	62	4.5	332	3	US-09-134-001C-5446	Sequence 5446, Ap
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1184	62.5	4.5	555	4	US-09-949-016-10036	Sequence 10036, A	1257	62	4.5	345	2	US-09-248-796A-27331	Sequence 27331, A
1185	62.5	4.5	555	4	US-09-583-110-3944	Sequence 3944, Ap	1258	62	4.5	345	2	US-08-758-621-14	Sequence 14, Appl
1186	62.5	4.5	595	4	US-09-107-433-3977	Sequence 3977, Ap	1259	62	4.5	345	4	US-09-107-858-14	Sequence 14, Appl
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1188	62.5	4.5	627	4	US-07-959-943-11	Sequence 11, Appli	1261	62	4.5	355	3	US-08-847-296B-1	Sequence 1, Appli
1189	62.5	4.5	630	1	US-07-959-943-11	Sequence 11, Appli	1262	62	4.5	355	3	US-09-045-583-54	Sequence 54, Appl
1190	62.5	4.5	630	4	US-09-622-503-1	Sequence 1, Appli	1263	62	4.5	355	4	US-09-534-185-54	Sequence 54, Appl
1191	62.5	4.5	649	3	US-08-800-291B-5	Sequence 5, Appli	1264	62	4.5	355	4	US-08-720-565-4	Sequence 4, Appli
1192	62.5	4.5	649	3	US-08-800-291B-6	Sequence 6, Appli	1265	62	4.5	355	4	US-10-039-659A-15	Sequence 15, Appl
1193	62.5	4.5	654	4	US-09-949-016-9301	Sequence 9301, Ap	1266	62	4.5	355	4	US-08-771-276-4	Sequence 4, Appli
1194	62.5	4.5	654	4	US-09-617-594A-4	Sequence 4, Appli	1267	62	4.5	355	4	US-08-375-199B-4	Sequence 4, Appli
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1270	62	4.5	365	4	US-09-503-219B-8	Sequence 8, Appli	1343	62	4.5	941	4	US-09-390-134B-31	Sequence 31, Appl
1271	62	4.5	374	4	US-09-248-796A-16046	Sequence 16046, A	1344	62	4.5	941	4	US-09-719-085A-2	Sequence 2, Appli
1272	62	4.5	385	4	US-09-198-452A-942	Sequence 942, App	1345	62	4.5	943	1	US-08-455-970A-10	Sequence 10, Appl
1273	62	4.5	390	4	US-09-107-532A-6052	Sequence 6052, Ap	1346	62	4.5	943	1	US-08-976-566-10	Sequence 10, Appl
1274	62	4.5	409	4	US-09-328-352-6044	Sequence 6044, Ap	1347	62	4.5	951	1	US-08-455-970A-14	Sequence 14, Appl
1275	62	4.5	412	4	US-09-489-039A-11599	Sequence 11999, A	1348	62	4.5	951	1	US-08-976-566-14	Sequence 14, Appl
1276	62	4.5	414	4	US-09-328-352-6961	Sequence 6961, Ap	1349	62	4.5	977	1	US-08-387-156-8	Sequence 8, Appli
1277	62	4.5	417	4	US-09-248-796A-20802	Sequence 20802, A	1350	62	4.5	977	2	US-08-694-865-8	Sequence 8, Appli
1278	62	4.5	422	4	US-09-489-039A-12531	Sequence 12531, A	1351	62	4.5	977	2	US-08-694-865-8	Sequence 8, Appli
1279	62	4.5	442	4	US-09-328-352-6055	Sequence 6055, Ap	1352	62	4.5	977	3	US-09-124-491-8	Sequence 8, Appli
1280	62	4.5	444	4	US-09-489-039A-9750	Sequence 9750, Ap	1353	62	4.5	977	3	US-09-383-913-8	Sequence 8, Appli
1281	62	4.5	445	4	US-09-710-279-2644	Sequence 2644, Ap	1354	62	4.5	980	1	US-08-091-569-2	Sequence 2, Appli
1282	62	4.5	446	4	US-09-949-016-10494	Sequence 10494, A	1355	62	4.5	980	1	US-08-203-676-2	Sequence 2, Appli
1283	62	4.5	462	3	US-08-788-231A-15	Sequence 15, Appl	1356	62	4.5	980	2	US-08-822-238-2	Sequence 2, Appli
1284	62	4.5	465	4	US-09-438-185A-878	Sequence 878, App	1357	62	4.5	1069	1	US-07-777-715-9	Sequence 9, Appli
1285	62	4.5	475	4	US-09-252-991A-29697	Sequence 29697, A	1358	62	4.5	1069	1	US-08-170-126-4	Sequence 4, Appli
1286	62	4.5	477	3	US-09-134-001C-3487	Sequence 3487, Ap	1359	62	4.5	1069	3	US-08-954-418-4	Sequence 4, Appli
1287	62	4.5	477	4	US-09-949-016-10716	Sequence 10716, A	1360	62	4.5	1098	1	US-07-777-715-7	Sequence 7, Appli
1288	62	4.5	483	4	US-09-107-532A-5650	Sequence 5650, Ap	1361	62	4.5	1098	1	US-08-170-126-2	Sequence 2, Appli
1289	62	4.5	488	2	US-08-928-692-10	Sequence 10, Appl	1362	62	4.5	1098	3	US-08-954-418-2	Sequence 2, Appli
1290	62	4.5	488	3	US-09-339-972-10	Sequence 10, Appl	1363	62	4.5	1509	4	US-09-676-519-27	Sequence 27, Appl
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1292	62	4.5	493	3	US-09-134-001C-3486	Sequence 3486, Ap	1365	62	4.5	2227	3	US-08-397-232-2	Sequence 2, Appli
1293	62	4.5	496	4	US-09-543-681A-6439	Sequence 6439, Ap	1366	62	4.5	2227	3	US-09-171-387-2	Sequence 2, Appli
1294	62	4.5	499	3	US-09-134-001C-5370	Sequence 5370, Ap	1367	62	4.5	2227	4	US-09-653-499-2	Sequence 2, Appli
1295	62	4.5	502	1	US-08-484-840-3	Sequence 3, Appli	1368	62	4.5	2227	4	US-10-104-966-12	Sequence 12, Appl
1296	62	4.5	502	1	US-08-483-094-3	Sequence 3, Appli	1369	62	4.5	2227	4	US-10-135-988-2	Sequence 2, Appli
1297	62	4.5	506	4	US-09-252-991A-23257	Sequence 23257, A	1370	62	4.5	2227	4	US-08-469-260A-401	Sequence 401, App
1298	62	4.5	511	4	US-09-107-532A-6112	Sequence 6112, Ap	1371	62	4.5	2227	4	US-08-469-260A-401	Sequence 401, App
1299	62	4.5	511	4	US-09-917-265A-67	Sequence 67, Appl	1372	62	4.5	2227	4	US-08-467-344A-401	Sequence 401, App
1300	62	4.5	512	4	US-09-540-236-3548	Sequence 3548, Ap	1373	62	4.5	2227	4	US-08-424-550B-401	Sequence 401, App
1301	62	4.5	519	4	US-09-786-240-3	Sequence 3, Appli	1374	61.5	4.4	143	4	US-09-270-767-34144	Sequence 34144, A
1302	62	4.5	533	4	US-09-917-265A-62	Sequence 62, Appl	1375	61.5	4.4	143	4	US-09-270-767-34144	Sequence 34144, A
1303	62	4.5	534	4	US-09-328-352-6713	Sequence 6713, Ap	1376	61.5	4.4	151	4	US-09-328-352-6429	Sequence 6429, Ap
1304	62	4.5	552	4	US-09-248-796A-20713	Sequence 20713, A	1377	61.5	4.4	168	4	US-09-583-110-3307	Sequence 3307, Ap
1305	62	4.5	579	4	US-09-529-279-4	Sequence 4, Appli	1378	61.5	4.4	177	4	US-09-248-796A-20689	Sequence 20689, A
1306	62	4.5	579	4	US-10-158-895-4	Sequence 4, Appli	1379	61.5	4.4	187	4	US-09-248-796A-20689	Sequence 20689, A
1307	62	4.5	590	4	US-09-529-279-15	Sequence 15, Appl	1380	61.5	4.4	200	4	US-09-270-767-35200	Sequence 35200, A
1308	62	4.5	590	4	US-10-158-895-15	Sequence 15, Appl	1381	61.5	4.4	200	4	US-09-270-767-50417	Sequence 50417, A
1309	62	4.5	633	4	US-09-949-016-9902	Sequence 9902, Ap	1382	61.5	4.4	204	3	US-09-053-197A-29	Sequence 29, Appl
1310	62	4.5	635	4	US-09-489-039A-13395	Sequence 13395, A	1383	61.5	4.4	204	3	US-09-085-761A-29	Sequence 29, Appl
1311	62	4.5	648	4	US-09-710-279-1060	Sequence 1060, Ap	1384	61.5	4.4	204	4	US-09-543-681A-6333	Sequence 6333, Ap
1312	62	4.5	654	4	US-08-979-847B-91	Sequence 91, Appl	1385	61.5	4.4	206	3	US-09-107-383-15	Sequence 15, Appl
1313	62	4.5	668	3	US-09-134-001C-3430	Sequence 3430, Ap	1386	61.5	4.4	206	4	US-09-643-914-15	Sequence 15, Appl
1314	62	4.5	681	4	US-09-583-110-5255	Sequence 5453, Ap	1387	61.5	4.4	206	4	US-09-742-361A-15	Sequence 15, Appl
1315	62	4.5	684	4	US-09-583-110-5255	Sequence 5255, Ap	1388	61.5	4.4	214	4	US-09-328-352-6025	Sequence 6025, Ap
1316	62	4.5	686	4	US-09-252-991A-19332	Sequence 19332, A	1389	61.5	4.4	219	2	US-08-751-767A-2	Sequence 2, Appli
1317	62	4.5	691	4	US-09-107-433-4260	Sequence 4260, Ap	1390	61.5	4.4	219	4	US-09-462-941-18	Sequence 18, Appl
1318	62	4.5	724	4	US-09-710-279-3082	Sequence 3082, Ap	1391	61.5	4.4	221	4	US-09-949-016-6001	Sequence 6001, Ap
1319	62	4.5	738	4	US-09-949-016-11165	Sequence 11165, A	1392	61.5	4.4	224	4	US-09-328-352-6659	Sequence 6659, Ap
1320	62	4.5	756	3	US-09-134-001C-3553	Sequence 3553, Ap	1393	61.5	4.4	224	4	US-09-393-634-9	Sequence 9, Appli
1321	62	4.5	768	4	US-08-979-847B-89	Sequence 89, Appl	1394	61.5	4.4	231	3	US-09-134-001C-4408	Sequence 4408, Ap
1322	62	4.5	770	4	US-09-252-991A-25267	Sequence 25267, A	1395	61.5	4.4	245	4	US-09-198-452A-1091	Sequence 1091, Ap
1323	62	4.5	785	4	US-09-134-000C-6690	Sequence 6690, Ap	1396	61.5	4.4	245	4	US-09-438-185A-1019	Sequence 1019, Ap
1324	62	4.5	801	4	US-09-710-279-2020	Sequence 2020, Ap	1397	61.5	4.4	253	4	US-09-134-000C-5058	Sequence 5058, Ap
1325	62	4.5	808	3	US-09-134-001C-3105	Sequence 3105, Ap	1398	61.5	4.4	275	4	US-09-803-671B-5	Sequence 5, Appli
1326	62	4.5	820	4	US-09-328-352-5766	Sequence 5766, Ap	1399	61.5	4.4	275	4	US-10-274-409-5	Sequence 5, Appli
1327	62	4.5	844	4	US-09-949-016-9438	Sequence 9438, Ap	1400	61.5	4.4	287	4	US-09-690-454-55	Sequence 55, Appl
1328	62	4.5	859	3	US-09-183-253-2	Sequence 2, Appli	1401	61.5	4.4	296	4	US-09-248-796A-23203	Sequence 23203, A
1329	62	4.5	924	3	US-08-619-812-8	Sequence 8, Appli	1402	61.5	4.4	297	1	US-07-866-560-4	Sequence 4, Appli
1330	62	4.5	926	1	US-07-908-253-2	Sequence 2, Appli	1403	61.5	4.4	297	1	US-08-077-673-4	Sequence 4, Appli
1331	62	4.5	926	1	US-08-455-970A-2	Sequence 2, Appli	1404	61.5	4.4	297	1	US-08-671-525B-4	Sequence 4, Appli
1332	62	4.5	926	1	US-08-387-156-6	Sequence 6, Appli	1405	61.5	4.4	297	1	US-08-672-109B-4	Sequence 4, Appli
1333	62	4.5	926	2	US-08-694-865-6	Sequence 6, Appli	1406	61.5	4.4	297	2	US-08-478-992-4	Sequence 4, Appli
1334	62	4.5	926	2	US-08-878-748-6	Sequence 6, Appli	1407	61.5	4.4	297	2	US-08-842-045-4	Sequence 4, Appli
1335	62	4.5	926	2	US-08-535-837-2	Sequence 2, Appli	1408	61.5	4.4	297	2	US-08-466-906B-7	Sequence 7, Appli
1336	62	4.5	926	3	US-09-124-491-6	Sequence 6, Appli	1409	61.5	4.4	297	2	US-08-842-238-4	Sequence 4, Appli
1337	62	4.5	926	4	US-09-383-912-6	Sequence 6, Appli	1410	61.5	4.4	297	3	US-08-780-749A-3	Sequence 3, Appli
1338	62	4.5	926	4	US-08-976-566-2	Sequence 2, Appli	1411	61.5	4.4	297	3	US-09-105-298-4	Sequence 4, Appli
1339	62	4.5	926	6	5476657-3	Patent No. 5476657	1412	61.5	4.4	297	3	US-08-629-335B-4	Sequence 4, Appli
1340	62	4.5	926	6	5476657-3	Patent No. 5476657	1413	61.5	4.4	297	3	US-09-201-746-7	Sequence 7, Appli
1341	62	4.5	936	1	US-08-455-970A-12	Sequence 12, Appl	1414	61.5	4.4	297	3	US-08-870-511-3	Sequence 3, Appli


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Db 181 HSGNFGTDLQKHLWNPEDKGYALHMTTAAEWSMSPSPFGFLTYIRDQKISLRVEAN 240
Qy 241 LHGLTYDTPACPNNRTRLLSRDI 266
Db 241 LHGLTYDTPACPNNRTRLLSRDI 266

RESULT 2
US-09-663-600A-96
; Sequence 96, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 96
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-663-600A-96

Query Match 42.8%; Score 595.5; DB 4; Length 172;
Best Local Similarity 79.4%; Pred. No. 2.1e-58;
Matches 123; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

Qy 1 MMWFQOGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MMWFQOGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Qy 61 NIAAVLCIATYVRYKQVHSAALFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 120
Db 61 NIAAVLCIATYVRYKQVHSAALFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 120
Qy 121 HV--SGAVLFGMSLYMFTQILSYQMPKIHCK 153
Db 121 TCKWSCAYLWYGL-IIYVCSDHPLPKCPKSNKG 154

RESULT 3
US-09-724-864-38
; Sequence 38, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James G
; APPLICANT: Murison, James G
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
```

```
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
; US-09-724-864-38

Query Match 34.4%; Score 479.5; DB 3; Length 238;
Best Local Similarity 37.3%; Pred. No. 3e-45;
Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;

Qy 1 MMWFQOGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MLCFLRGMAFVPLLVLTWSSAAFIISYVAVLSGHVNPFLPYISDTGTTPPSGGIFGFM 60
Qy 61 NIAAVLCIATYVRYKQV-----HALSPEENVIIKLNKAGLVGLSCLGLSIVANFQ 113
Db 61 NFSAFGLAATWYTRYKIVEKQNETCYFSTPVFNLV-----SLALGLVCGIGMGIIVANFQ 114
Qy 114 KTTLFAAHVSGAVLTFMGSLYMFVTILSYQMPKIHQKQVFWIRLLVIMCGVSAISM 173
Db 115 ELAVPVVHDGALLAFVCGVYVTLQSIISYKSCQWNSLTTCVHMAISAVSAAVWPM 174
Qy 174 LTCSSVLHSGNFGTDLQKHLWNPEDKGYVLMHTTAAEWSMSPSPFGFLTYIRDFOKI 233
Db 175 IACASLISI-----TKLEWNPKEKDIYHVVSACEWTVAFGFIYFLTFIQDFQSV 226
Qy 234 SLRVEANLH 242
Db 227 TLRISTEIN 235

RESULT 4
US-09-663-600A-130
; Sequence 130, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 130
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-663-600A-130

Query Match 25.7%; Score 358; DB 4; Length 69;
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Best Local Similarity 100.0%; Pred. No. 1.9e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWMFQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWMFQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Qy 61 NIAAVLC 67
Db 61 NIAAVLC 67

RESULT 5
US-09-663-600A-224
; Sequence 224, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 224
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-663-600A-224

Query Match 25.7%; Score 358; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.9e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWMFQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWMFQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Qy 61 NIAAVLC 67
Db 61 NIAAVLC 67

RESULT 6
US-08-905-223-20
; Sequence 20, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:

; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 1..21
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-08-905-223-20

Query Match 8.5%; Score 118; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWMFQGLSFLPSALVIWTS/AF 21
Db 1 MWMFQGLSFLPSALVIWTS/AF 21

RESULT 7
US-09-247-155-20
; Sequence 20, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 20
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens

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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-09-247-155-20

Query Match      8.5%; Score 118; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWFQOGLSFLPSALVIWTS 21
Db 1 MMWFQOGLSFLPSALVIWTS 21

RESULT 8
US-09-663-600A-20
; Sequence 20, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueloret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663.600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 20
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-09-663-600A-20

Query Match      8.5%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWFQOGLSFLPSALVIWTS 21
Db 1 MMWFQOGLSFLPSALVIWTS 21

RESULT 9
US-09-621-976-2
; Sequence 2, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21..-1
US-09-621-976-2

Query Match      8.5%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWFQOGLSFLPSALVIWTS 21
Db 1 MMWFQOGLSFLPSALVIWTS 21

RESULT 10
US-09-513-999C-2
; Sequence 2, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-09-513-999C-2

Query Match      8.5%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWFQOGLSFLPSALVIWTS 21
Db 1 MMWFQOGLSFLPSALVIWTS 21

RESULT 11
US-09-471-276-2
; Sequence 2, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A. J.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
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; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SPLPSALVIWTS/AF
US-09-471-276-2

Query Match      8.5%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWWFQOGLSFLPSALVIWTS 21
| | | | | | | | | | | | | | | | | | | | |
Db 1 MWWFQOGLSFLPSALVIWTS 21

RESULT 12
US-09-107-532A-4147
; Sequence 4147, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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```
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...291
; SEQUENCE DESCRIPTION: SEQ ID NO: 4147:
US-09-107-532A-4147

Query Match      6.6%; Score 91.5; DB 4; Length 291;
Best Local Similarity 22.9%; Pred. No. 0.088;
Matches 58; Conservative 26; Mismatches 88; Indels 81; Gaps 9;

Qy 6 QGLSFLPSALV-----IWTSAAFIRSYITAVTLHHDDPALPYISDGTGVAPEKCLFGAM 59
| | | | | | | | | | | | | | | | | | | | |
Db 51 RGMSLMGDAISHAVLPGVAISYMFSGYIFGAT-----AFGML 88

Qy 60 LNTAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLSIYANFQKTT--- 116
| | | | | | | | | | | | | | | | | | | | |
Db 89 --TAAVIGFVTSRLKNDTAI-----GIVFSSFFALGIIILISYAQSATDLY 133

Qy 117 -----LPAHVSGAVLTFMGSLYMFVQTILSYQMOP---KIHKQVFWI 158
| | | | | | | | | | | | | | | | | | | | |
Db 134 HILFGNVLAVRESDLLLTALVSGVILIP-----VFFYKELKITSFDPMTAKAYGLNTSLI 189

Qy 159 RLLLVIVCGVSALSMLTCSVLHSGNFGTDLQKLNHPEDKGY-----VLHMITTAAEW 213
| | | | | | | | | | | | | | | | | | | | |
Db 190 HYLLMFF-----LTLVAVSLQTVGTILVILAMITPAATAYLLTNHLLKMLITANGI 241

Qy 214 SMSFSFFGFELTY 226
| | | | |
Db 242 GMLSAVVGVEFSY 254

RESULT 13
US-09-721-870-14
; Sequence 14, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-14

Query Match      6.6%; Score 91.5; DB 4; Length 387;
Best Local Similarity 23.0%; Pred. No. 0.13;
Matches 50; Conservative 34; Mismatches 82; Indels 51; Gaps 11;

Qy 69 ATIVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLSIYANFQKTTLFAAH----- 121
| | | | | | | | | | | | | | | | | | | | |
Db 46 AVLYLTWKH-RQLQTVQNIFILNCASNVLMLCITSLPITFITVYKQWFFSSPVCKLIPL 104

Qy 122 VSGA---VLTFGMSLYMFVQTILSYQMOPKIHKQVFTIRLLLVIVCGVSALSMLTCS 178
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Db 105 VQGASIFVSTFSLSAIALDRYNLVVRPHKQKLSRSAMMIALL--IW-----VISVVVCM 158

Qy 179 VLHSGNFGTDLE-QKL-----HWNPED--KGYVLHMITTAAEWSMSFSFFGFFLT 225
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Db 159 -----YGYTMDVEKLNGLCGEYCSBHWPLAEVRKGTFTFLVLIT-----QLFPFATWAF 208

Qy 226 YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLL 262
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Db 209 YNIFSLRQRVEYKXKL-----SERSQLL 234 :||:|

RESULT 14

US-09-602-787A-588

Sequence 588, Application US/09602787A

Patent No. 6696561

GENERAL INFORMATION:

APPLICANT: Pompejus, Mark

APPLICANT: Kr"ger, Burkhard

APPLICANT: Sch"der, Hartwig

APPLICANT: Zelder, Oskar

APPLICANT: Heberhauer, Gregor

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS

TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE

TITLE OF INVENTION: TRANSPORT

FILE REFERENCE: BGI-125CP

CURRENT APPLICATION NUMBER: US/09/602,787A

CURRENT FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: USSN 60/141031

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: DE 19931454.3

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: DE 19931478.0

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: DE 19931563.9

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: DE 19932122.1

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932124.8

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932180.9

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932182.5

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932190.6

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932191.4

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932209.0

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932212.0

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932227.9

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932228.7

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932229.5

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932230.9

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932927.3

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19933005.0

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19933006.9

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19940764.9

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: DE 19940765.7

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: DE 19940766.5

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: DE 19940830.0

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: DE 19940831.9

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: DE 19940832.7

Query Match 6.5%; Score 90; DB 4; Length 283;

Best Local Similarity 23.8%; Pred. No. 0.12;

Matches 46; Conservative 33; Mismatches 64; Indels 50; Gaps 7;

QY 9 SFLPSALVITWTSAAFIYSY-----ITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLN-- 61

Db 76 ALIMSAGVVTWTSKSLSDVSIGLQFITMLSLGVVIVSHSDSHAVDLTSLFGDILGVR 135

QY 62 -----IAAVLCIATIVRYKQVHALSPEENV--IINKKAGLVGLSCLGSLIVAN 111

Db 136 PSDIFIATATVLGLTIFLHRQFTALAFDERKHAHTLGNPRFAHLMLALATATVVS 195

QY 112 FQKTTLFAAHVSGAVLTFCM-----GSLYMFQVITLSYQMPKIHGKQVFWIRLLIVWC 166

Db 196 FQ-----VVGTLVFGLLIGPPATAALLVQDKAS-----ISLMIV-- 231

QY 167 GVSALSMLTCSSV 179

Db 232 ----ASLLGCAEI 240

RESULT 15

US-09-248-796A-20434

Sequence 20434, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 20434

LENGTH: 396

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-20434

Query Match 6.5%; Score 90; DB 4; Length 396;

Best Local Similarity 20.5%; Pred. No. 0.2;

Matches 60; Conservative 35; Mismatches 90; Indels 108; Gaps 13;

QY 1 MMWFQGLSFLPSALVITWTSAAFIYSYITAVTLH-----HTDP-----A 39

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Db 65 LWWPWIFWLLSIGCVLTIISMI--YIPITHHKLSESYSEFFKRIDPLGLTGTGIIGLIL 122
Qy 40 LPYISDTGTVAPEKCLFGAMLNIAVLCIATIVV--RYKQVHALSPEE----- 85
Db 123 FNFVWTQGPVVGWNTAYIIALLIIIVAFFIIELYIAKYPLVPKSVFNKIGMVLAC 182
Qy 86 -----NVIKLNK-----AG-----LVLGILSCLGLSIVANFQKTTLF 118
Db 183 ISCGMGSGFIWQYYWNIIILNLRKYPTIAGSLTYVPFLVWGIIAAIASSIIISHTKPSYI 242
Qy 119 AAHVSGAVLTFMGSLYMFVQTILSYQMPKIHKQVFWIRLLL---VWCGVSALSMLT 175
Db 243 ---ISFSTICFMVGCMLSVTPI-----QOSYFRLTLGQMFILCWAMDMSFPA 287
Qy 176 CSSVL-----HSGNCTDLEQKLHNWNPEDKGYVLHMITTAAEWSMSFSFPG 221
Db 288 ASIILSDYLPNHQMGAGS-----LVSTVINYSVSL-PLG 321
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Job time : 58 secs

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OM protein - protein search, using sw model

Run on: August 26, 2005, 17:21:42 ; Search time 164 Seconds
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637.307 Million cell updates/sec

Perfect score: 1392

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Searched: 1767149 seqs, 392926209 residues

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Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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31	1392	100.0	266	10	US-09-974-879-147
563	1392	100.0	266	14	US-10-174-587-10
627	1392	100.0	266	14	US-10-063-742-2
733	1392	100.0	266	15	US-10-264-237-2714
737	1392	100.0	266	15	US-10-621-401-147
744	1392	100.0	266	17	US-10-972-317-2
746	1392	100.0	267	10	US-09-305-736-147
747	1392	100.0	267	10	US-09-818-683-147
748	1392	100.0	267	11	US-09-818-683-147
749	1392	100.0	275	15	US-10-276-774-2411
750	1388	99.7	267	11	US-09-978-360A-702

SUMMARIES

1388	99.7	267	14	US-10-319-763-190	Sequence 190, App
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480.5	34.5	231	15	US-10-415-188-11	Sequence 11, Appl
461.5	33.2	246	15	US-10-243-552-975	Sequence 975, App
358	25.7	69	11	US-09-978-360A-736	Sequence 736, App
358	25.7	69	14	US-10-319-763-130	Sequence 130, App
358	25.7	69	14	US-10-319-763-224	Sequence 224, App
317.5	22.8	180	15	US-10-264-237-2144	Sequence 2144, Ap
251	18.0	132	16	US-10-755-889-453	Sequence 453, App
251	18.0	132	16	US-10-643-795A-100	Sequence 100, App
251	18.0	132	17	US-10-948-518-100	Sequence 100, App
214.5	15.4	283	15	US-10-243-552-521	Sequence 521, App
212	15.2	249	18	US-10-712-892A-37	Sequence 37, Appl
152	10.9	304	15	US-10-131-487A-83	Sequence 83, Appl
151.5	10.9	437	10	US-09-374-046A-66	Sequence 66, Appl
151.5	10.9	437	15	US-10-616-263-66	Sequence 66, Appl
126	9.1	63	15	US-10-243-552-618	Sequence 618, App
118	8.5	21	10	US-09-903-190-20	Sequence 20, Appl
118	8.5	21	14	US-10-319-763-20	Sequence 20, Appl
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105	7.5	218	14	US-10-050-704-322	Sequence 322, App
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105	7.5	220	14	US-10-050-704-309	Sequence 309, App
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89	6.4	757	14	US-10-168-428-4	Sequence 4, Appl
89	6.4	1203	15	US-10-311-623-3	Sequence 3, Appl
88.5	6.4	372	15	US-10-094-749-2651	Sequence 2651, Ap
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88	6.3	909	16	US-10-437-963-151932	Sequence 151932, App
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87.5	6.3	453	15	US-10-096-625-117	Sequence 117, App
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827	85	6.1	265	20	US-11-006-098-46	Sequence 46, Appl	1491	82	5.9	299	10	US-03-510-332-81	Sequence 81, Appl
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830	85	6.1	384	16	US-10-437-963-167436	Sequence 167436	1494	82	5.9	299	16	US-10-770-127-81	Sequence 81, Appl
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832	85	6.1	419	9	US-09-738-626-4556	Sequence 4556, Ap	1496	82	5.9	417	15	US-10-282-122A-56081	Sequence 56081, A
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834	85	6.1	498	9	US-09-949-145-4	Sequence 4, Appli	1498	82	5.9	451	16	US-10-425-115-207918	Sequence 207918,
835	85	6.1	498	9	US-10-074-978A-245	Sequence 245, App	1499	82	5.9	471	15	US-10-424-599-255264	Sequence 255264,
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876	83	6.0	321	15	US-10-005-041A-83	Sequence 83, Appl							
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878	83	6.0	321	15	US-10-343-650A-664	Sequence 664, App							
879	83	6.0	321	16	US-10-618-281-76	Sequence 76, Appl							
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884	83	6.0	1635	17	US-10-732-923-1745	Sequence 1745, Ap							
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887	83	6.0	2159	16	US-10-739-930-7476	Sequence 7476, Ap							
888	82.5	5.9	391	15	US-10-369-493-22053	Sequence 22053, A							
889	82.5	5.9	395	15	US-10-282-122A-55935	Sequence 55935, A							
890	82.5	5.9	431	17	US-10-732-923-23925	Sequence 23925, A							
891	82.5	5.9	451	14	US-10-156-761-12891	Sequence 12891, A							
892	82.5	5.9	452	15	US-10-335-977-5393	Sequence 5393, Ap							
893	82.5	5.9	461	15	US-10-335-977-5394	Sequence 5394, Ap							
894	82.5	5.9	596	15	US-10-369-493-1465	Sequence 1465, Ap							
895	82.5	5.9	695	16	US-10-437-963-129260	Sequence 129260,							
896	82.5	5.9	1457	16	US-10-408-765A-1010	Sequence 1010, Ap							

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Job time : 183 secs

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